

10-07-11 10:07:31

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2005, 09:35:34 ; Search time 39 Seconds

(without alignments)

61.677 Million cell updates/sec

Title: SEO1
Perfect score: 105
Sequence: 1 axaaeakyaakyaaeakakaxa 25

Scoring table: BLOSUM6DDX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : PIR 79.4
1: pir1; *
2: pir2; *
3: pir3; *
4: pir4; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	67.6	924	2 T06635	hypothetical protein
2	65	61.9	168	2 T34804	hypothetical protein
3	63	60.0	179	2 F97683	50S ribosomal protein
4	63	60.0	179	2 AR2908	50S ribosomal protein
5	63	60.0	179	2 JV0057	ribosomal protein - E. coli
6	60	57.1	177	2 E87294	ATP synthase F0, B
7	58	55.2	354	1 GNWXR	ATP synthase F0, B
8	58	55.2	375	2 AT1625	ATP synthase F0, B
9	57	54.3	394	2 F90725	ATP synthase F0, B
10	57	54.3	394	2 G95576	ATP synthase F0, B
11	57	54.3	909	2 T06635	hypothetical protein
12	56	53.3	101	2 H59099	hypothetical protein
13	56	53.3	228	2 E87612	hypothetical protein
14	56	53.3	347	2 E83525	hypothetical protein
15	56	53.3	356	2 A88152	hypothetical protein
16	56	53.3	592	1 IKRBCA	hypothetical protein
17	56	53.3	97	2 S02376	hypothetical protein
18	55	52.4	110	2 T37490	hypothetical protein
19	55	52.4	555	2 S04909	hypothetical protein
20	55	52.4	1110	2 A51116	hypothetical protein
21	55	52.4	1147	2 T35781	hypothetical protein
22	55	52.4	1203	2 C95229	hypothetical protein
23	54.5	51.9	1216	2 G98093	hypothetical protein
24	54.5	51.9	1216	2 A62721	hypothetical protein
25	54	51.4	217	2 T34809	hypothetical protein
26	54	51.4	310	2 T07064	hypothetical protein
27	54	51.4	643	1 T34852	hypothetical protein
28	54	51.4	1156	2 A39638	hypothetical protein
29	54	51.4	4687	1 A39638	hypothetical protein

ALIGNMENTS

RESULT 1
T06635
hypothetical protein T20K18_130 - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06635
R;Bevan, M.; Peters, S.A.; van Steveren, M.; Dirksen, W.; Stiekema, W.; Bancroft, I.; Meuwissen, H.; Reference number: 215790
A;Accession: ATSP:T20K18_130
A;Gene: ATSP:T20K18_130
A;Map position: 4
A;Residues: 1-924 <BEV>
A;Cross-references: UNIPROT:Q9SU08; EMBL:AL049640; GSPDB:GN00062; ATSP:T20K18_130
C;Genetics:
A;Experimental source: cultivar Columbia; BAC clone T20K18_130
A;Map position: 4
A;Introns: 209/2; 699/3; 753/3; 785/2; 807/2; 853/3; 912/3
Query Match 1: 67.6%; Score 71; DB 2; Length 924; Best Local Similarity 67.6%; Score 71; DB 2; Length 924; Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
RESULT 2
T34804
hypothetical protein SC2E1_36 SC2E1_36 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Accession: T34804
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34804
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A;Reference number: 221557
A;Accession: T34804
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-168 <MUR>
A;Cross-references: UNIPROT:069907; EMBL:AL023797; PIDN:CAA19411.1; GSPDB:GN00070; SC08D1
A;Experimental source: strain A3 (2)
C;Genetics:
A;Gene: SC08D1; SC2E1_36
Query Match 1: 61.9%; Score 65; DB 2; Length 168; Best Local Similarity 62.5%; Pred. No. 0.81; Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 106 AEAKEAKAAKAAKKAAP 129
RESULT 3
 F97683 50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C;Species: Agrobacterium tumefaciens
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: F97683
 R;Fodder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourolo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: F97683
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-179 <LEV>
 A;Cross-references: UNIPROT:Q8UBZS; GB:AE007869; PIDN:AAK88423; 1; PID:915157917; GSPDB:G
 C;Genetics:
 A;Gene: AGR_C_4900
 A;Map position: circular chromosome
 C;Superfamily: Escherichia coli ribosomal protein L19
 Query Match 60.0%; Score 63; DB 2; Length 179;
 Best Local Similarity 69.2%; Pred. No. 1.4;
 Matches 18; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
Qy 1 AXAAEAKAKYAAE-AAKKAAX 24
Db 149 AQALAAEKAEEAABKAABEAKAA 174

RESULT 4
 AP2908 50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AP2908
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.; Erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McClellan, Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kressan, W.; Perry, M.; Gordon-Kamm, M.; Steiner, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AP2908
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-179 <KTR>
 A;Cross-references: UNIPROT:Q8UBZS; GB:AE008688; PIDN:AAL43684; 1; PID:917741210; GSPDB:G
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: rplS
 A;Map position: circular chromosome
 C;Superfamily: Escherichia coli ribosomal protein L19
 Query Match 60.0%; Score 63; DB 2; Length 179;
 Best Local Similarity 69.2%; Pred. No. 1.4;
 Matches 18; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
Qy 1 AXAAEAKAKYAAE-AAKKAAX 24
Db 149 AQALAAEKAEEAABKAABEAKAA 174

RESULT 5
 JV0057 tola protein - Escherichia coli (strain K-12)
 C;Species: Escherichia coli
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C;Accession: JV0057; B64810

Db 110 ASAEEAERQAKEEAVLAKLAAEA 134

RESULT 6
 E87294 4TP synthase F0, B' subunit [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: E87294
 R;Nierman, W.C.; Reldyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolonay, N. J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: E87294
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-177 <STO>
 A;Cross-references: UNIPROT:Q9AB65; GB:AE005673; NID:913421521; PIDN:AAK22353; 1; GSPDB:G
 C;Genetics:
 A;Gene: CC0366

Db 110 ASAEEAERQAKEEAVLAKLAAEA 134

RESULT 7
 GNVISR genome polyprotein 1 - tomato ringspot virus (strain raspberry) (fragment)
 C;Species: tomato ringspot virus

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: A40787
 C;Rott, M.E.; Tremaine, J.H.; Rochon, D.M.
 C;Title: Comparison of the 5' and 3' termini of tomato ringspot virus RNA1 and RNA2: evidence for a poly-A tail
 C;Accession: A40787
 C;Molecule type: genomic RNA
 C;Residues: 1-134 <ROT>
 C;Cross-references: UNIPROT:P29150; GB:N73822; NID:9335267; PIDN:AAA47941.1; PID:9555406
 C;Genetics:
 A;Map position: segment 1
 C;Superfamily: tomato ringspot virus genome polyprotein
 C;Keywords: glycoprotein; polyprotein
 C;Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 55.2%; Score 58; DB 1; Length 354;
 Best Local Similarity 70.0%; Pred. No. 9.7;
 Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Qy 6 REKAAYKAAYAAEAKAKAXA 25
 Db 180 ARKAAYKAAYAAEAKAKAXA 199

RESULT 8
 A71625
 rifin PFB0035C - malaria parasite (Plasmodium falciparum)
 C;Species: Plasmodium falciparum
 C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
 C;Accession: A71625
 R;Gardner, M.J.; Tettelin, H.; Casucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
 Peverte, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
 Science 282, 1126-1132, 1998
 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A;Reference number: A71600; PMID:99021743; PMID:9804551.
 A;Accession: A71625
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Residues: 1-375 <GAR>
 A;Cross-references: UNIPROT:096113; GB:AE001367; GB:AE001362; NID:93845074; PIDN:AACT179
 A;Experimental source: clone 3D7
 C;Genetics:
 A;Gene: PFB0035C
 C;Superfamily: Plasmodium falciparum rifin PFB1005W

Query Match 55.2%; Score 58; DB 2; Length 375;
 Best Local Similarity 56.5%; Pred. No. 10;
 Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Qy 2 XEAEEAKAKAYAAEAKAKAX 24
 Db 292 IVEGABQAKAKAAEKGVTAA 314

RESULT 9
 F90725
 membrane spanning protein Tola [imported] - Escherichia coli (strain 0157:H7, substrain
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: F90725
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic
 A;Reference number: A96529; MUID:1156331; PMID:11258756
 A;Accession: F90725
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-139 <HAY>
 A;Cross-references: UNIPROT:Q8X965; EMBL:AL049610; GSPDB:GN00062; ATSP:T20K18.120
 A;Experimental source: strain 0157:H7, substrain RIMD 050952
 C;Genetics:

A;Gene: EC80774
 Query Match 54.3%; Score 57; DB 2; Length 394;
 Best Local Similarity 56.0%; Pred. No. 14;
 Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 AXAAEAKAKAYAAEAKAKAX 25
 Db 151 ADDKAEEAKAKAADAKKKAEEA 175

RESULT 10
 G85576
 membrane spanning protein Tola [imported] - Escherichia coli (strain 0157:H7, substrain
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: G85576
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, J.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca, A.;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: G85576
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-394 <STO>
 A;Cross-references: UNIPROT:Q8X965; GB:AE005174; NID:912513672; PIDN:AACT55075.1; GSPDB:G
 A;Experimental source: strain 0157:H7, substrain EDL933
 C;Genetics:
 A;Gene: tola
 Query Match 54.3%; Score 57; DB 2; Length 394;
 Best Local Similarity 56.0%; Pred. No. 14;
 Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 AXAAEAKAKAYAAEAKAKAX 25
 Db 151 ADDKAEEAKAKAADAKKKAEEA 175

RESULT 11
 T06635
 hypothetical protein T20K18.120 - Arabidopsis thaliana (mouse-ear cress)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T06635
 R;Bevan, M.; Peters, S.A.; van Slaveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Meuwissen, M.; Reference number: Z15790
 A;Accession: T06635
 A;Residues: 1-903 <BEV>
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q9SU09; EMBL:AL049610; GSPDB:GN00062; ATSP:T20K18.120
 A;Experimental source: cultivar Columbia; BAC clone T20K18
 C;Genetics:
 A;Gene: ATSP:T20K18.120
 A;Map position: 4
 A;Introns: 205/2; 686/3; 740/3; 772/2; 808/3; 838/3; 897/3
 Query Match 54.3%; Score 57; DB 2; Length 909;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 AXAAEAKAKAYAAEAKAX 21
 Db 593 AHAEARERAAAGAERKA 613

RESULT 12
 H50989
 hypothetical protein px01-72 - Bacillus anthracis virulence plasmid px01
 C;Species: Bacillus anthracis
 C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

Db	542	EAIAEAKAKKAASKSSAK	562
RESULT 17			
IKEBCA			
C;Species: <i>Citrobacter freundii</i>			
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004			
C;Accession: I40784; A03504; I40777			
A;Molecule type: DNA			
A;Residues: 1-592 <RES>			
A;Cross-references: UNIPROT:P04480; GB:M37402; NID:9144661; PIDN:AAAT2879.1; PID:9144667			
A;Experimental source: plasmid ColA			
R;Morlon, J.; Lloubes, R.; Vareigne, S.; Chartier, M.; Lazdunski, C.			
J. Mol. Biol. 170, 271-285, 1983			
A;Title: Complete nucleotide sequence of the structural gene for colicin A, a gene transcribed from the ColA promoter			
A;Reference number: A03504; MUID:84036205; PMID:6313941			
A;Accession: A03504			
A;Molecule type: DNA			
A;Residues: 1-592 <MOR>			
A;Reference number: I40777; MUID:84057757; PMID:6641715			
A;Accession: I40777			
A;Status: translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-53, 'X', 55-70 <RE2>			
A;Cross-references: GB:M26369; NID:9144659; PIDN:AA98057.1; PID:9144660			
A;Experimental source: plasmid ColA			
A;Status: translated from GB/EMBL/DBJ			
C;Comment: This protein acts to depolarize the bacterial inner membrane, most likely by			
A;Gene: caa			
A;Genome: Plasmid			
C;Superfamily: colicin IB			
C;Keywords: antibiotic; bacteriocin; toxin; transmembrane protein			
RESULT 18			
SO4376			
antifreeze protein precursor - yellowtail flounder			
C;Species: <i>Limanda ferruginea</i> (yellowtail flounder)			
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004			
C;Accession: S02376			
R;Scott, G.K.; Davies, P.L.; Shears, M.A.; Fletcher, G.L.			
Eur. J. Biochem. 168, 629-633, 1987			
A;Title: Structural variations in the alanine-rich antifreeze proteins of the Pleuronectidae			
A;Reference number: S02376; MUID:88029483; PMID:3665537			
A;Accession: S02376			
A;Molecule type: mRNA			
A;Residues: 1-97 <SCO>			
A;Cross-references: UNIPROT:P09031; EMBL:X06356; NID:96401; PIDN:CAA29655.1; PID:964042			
A;Note: part of this sequence, including the amino end of the mature protein, was confirmed			
C;Superfamily: antifreeze protein			
C;Keywords: antifreeze			
RESULT 19			
T37490			
ribosomal protein rpa6 - fission yeast (<i>Schizosaccharomyces pombe</i>)			
C;Species: <i>Schizosaccharomyces pombe</i>			
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004			
C;Accession: T37490			
R;Bottie, G.; Pohl, T.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.			
Submit to the EMBL Data Library, November 1999			
A;Reference number: Z21718			
A;Accession: T37490			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-110 <B0T>			
A;Cross-references: UNIPROT:O14317; EMBL:AL132769; PIDN:CA59884.1; GSPDB:GN00066; SFDB			
A;Experimental source: strain 972h-; cosmid c1071			
C;Genetics:			
A;Gene: SPDB:SPAC1071.08			
A;Map position: 1			
A;Introns: 10/3			
C;Superfamily: rat acidic ribosomal protein P1			
RESULT 20			
SO4909			
embryonic protein DC8 (clone 8/10) - carrot			
C;Species: <i>Daucus carota</i> (carrot)			
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004			
C;Accession: S04909			
R;Franz, G.; Hatzopoulos, P.; Jones, T.J.; Krauss, M.; Sung, Z.R.			
Mol. Gen. Genet. 218, 143-151, 1989			
A;Title: Molecular and genetic analysis of an embryonic gene, DC 8, from <i>Daucus carota</i>			
A;Reference number: S04909; MUID:8938429; PMID:2571069			
A;Accession: S04909			
A;Status: not compared with conceptual translation			
A;Molecule type: DNA			
A;Residues: 1-155 <FRA>			
A;Cross-references: UNIPROT:P20075; GB:X16131; NID:91833; PIDN:CRA34258.2; PID:9490246			
C;Superfamily: pea seed biotin-containing protein			
RESULT 21			
15116			
NF-88 - sea lamprey			
C;Species: <i>Petromyzon marinus</i> (sea lamprey)			

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: I51116
 R;Jacobs, A.J.; Kamholz, J.; Selzer, M.E.
 Brain Res. Mol. Brain Res. 29, 43-52, 1995
 A;Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation re
 A;Reference number: I51116; MUID:9528814; PMID:770000
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1110 <JAC>
 A;Cross-references: UNIPROT:091255; EMBL:U19361; NID:9632548; PIDN:AAA80106.1; PID:g6325
 C;Superfamily: neurofilament triplet H protein
 A;Accession: 1-1110 <JAC>
 Query Match 52.4%; Score 55; DB 2; Length 1110;
 Best Local Similarity 65.0%; Pred. No. 57; Mismatches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AXAAEAKAKYAAEAKA 20
 DB 725 AEAAEAEAKSEBEEA 744
 RESULT 22
 T5781 hypothetical protein SC8A6_14c SC8A6_14c - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C;Accession: T35781
 R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, July 1998
 A;Reference number: 221570
 A;Accession: T35781
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1147 <SEE>
 A;Cross-references: UNIPROT:087848; EMBL:AL031013; PIDN:CAA19796.1; GSPDB:GN00070; SCOB
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: SCOB:SC8A6_14c
 Query Match 52.4%; Score 55; DB 2; Length 1147;
 Best Local Similarity 50.0%; Pred. No. 59; Mismatches 12; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 AXAAEAKAKYAAEAKAKA 24
 DB 264 AEAAQAEQDVQSRARAANKKARAA 287
 RESULT 23
 C95229 DNA-directed RNA polymerase, beta chain [imported] - Streptococcus pneumoniae (strain T1
 C;Species: Streptococcus pneumoniae
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C;Accession: C95229
 R;Tettelein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 Nelson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number: A95000; MUID:21357209; PMID:11463916
 A;Accession: C95229
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1203 <KUR>
 A;Cross-references: UNIPROT:Q97NQ7; GB:AE005672; PIDN:AAK76028.1; PID:g14973467; GSPDB:G
 A;Experimental source: strain TIGR4
 C;Genetics:
 A;Gene: SPI961
 C;Superfamily: DNA-directed RNA polymerase beta chain
 Query Match 51.9%; Score 54.5; DB 2; Length 1203;
 Best Local Similarity 53.8%; Pred. No. 70; Mismatches 14; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
 QY 1 AXAAEAKAKYAAEAKAKA 25
 DB 1170 AREKAAQEAKAAEAEAKATAKA 1195
 RESULT 24
 G98093 DNA-directed RNA polymerase (EC 2.7.7.6) [imported] - Streptococcus pneumoniae (strain R6
 C;Species: Streptococcus pneumoniae
 C;Accession: G98093
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Be
 e, R.; LeBlanc, D.J.; Lee, L.N.; Leffkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
 Y, P.; Sun, P.M.; Winkler, M.E.; Bacteriol. 183, 5705-5717, 2001
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A97872; MUID:21429245; PMID:1154234
 A;Accession: G98093
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q8DNE0; GB:AE007317; PID:g15459460; GSPDB:GN
 C;Genetics:
 A;Gene: rpoB
 C;Superfamily: DNA-directed RNA polymerase beta chain
 C;Keywords: nucleotidyltransferase
 Query Match 51.9%; Score 54.5; DB 2; Length 1216;
 Best Local Similarity 53.8%; Pred. No. 70; Mismatches 14; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
 QY 1 AXAAEAKA-AKVAEAAEAKAKA 25
 DB 1183 AREKAQAEKAFAEEAEAKATAKA 1208
 RESULT 25
 A26721 histone H1-gamma, embryonic - sea urchin (Strongylocentrotus purpuratus)
 C;Species: Strongylocentrotus purpuratus (purple urchin)
 C;Date: 19-Nov-1998 #sequence_revision 19-Nov-1998 #text_change 09-Jul-2004
 C;Accession: A26721
 R;Knowles, J.A.; Lai, Z.C.; Chidts, G.J.
 Mol. Cell. Biol. 7, 478-485, 1987
 A;Title: Isolation, characterization, and expression of the gene encoding the late histon
 A;Reference number: A26721; MUID:87172742; PMID:3031476
 A;Accession: A26721
 A;Molecule type: DNA
 A;Residues: 1-217 <KNO>
 A;Cross-references: UNIPROT:R07796; GB:MI6033; NID:9161517; PIDN:AAA30059.1; PID:g161518
 C;Superfamily: histone H1
 C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
 P;2-217/Product: histone H1-gamma, embryonic #status predicted <MAT>
 Query Match 54.2%; Score 54; DB 2; Length 217;
 Best Local Similarity 54.2%; Pred. No. 18; Mismatches 13; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 AXAAEAKAKYAAEAKAKA 24
 DB 189 AAAKPAKKAQPKAKPKAKKA 212
 RESULT 26
 T34809 ribosomal protein S2 - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C;Accession: T34809

A;Reference: T34509; Status: preliminary; Residues: 1-310; Molecule type: DNA; Cross-references: UNIPROT:Q31212; EMBL:AL023797; PIDN:CAM19416.1; GSPDB:GN00070; SCOP: C; Gene: rpsB; Superfamily: Escherichia coli ribosomal protein S2	Query Match 51.4%; Score 54; DB 2; Length 310; Best Local Similarity 51.3%; Pred. No. 25; Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0; Oy 2 XAEAAEKAKYAAEAAEKAKAXA 25 Db 281 AAEAAEAAPEAAPEPEAAEAPA 304	RESULT 27
seed biotin-containing protein LEA [validated] - soybean		TO7064
C;Species: Glycine max (soybean)		
C;Date: 01-Sep-2000 #sequence_revision 01-Sep-2000 #text_change 09-Jul-2004		
C;Accession: T07064		
R;Haing, Y.C.; Tsou, C.H.; Hsu, T.F.; Chen, Z.Y.; Hsieh, K.L.; Hsieh, J.S.; Chow, T.Y.		
Plant Mol. Biol. 38, 491-490, 1998		
A;Title: Tissue- and stage-specific expression of a soybean (Glycine max L.) seed-mature		
A;Reference number: Z15895; MUID:98416627; PMID:9747055		
A;Accession: T07064		
A;Status: preliminary; Residues: 1-643 <HST>		
A;Cross-references: UNIPROT:Q39846; EMBL:U59626; PIDN:G1389896; PIDN:AC61783.1; PID:9138		
A;Experimental source: strain Shi-Shi; cotyledon		
C;Superfamily: pea seed biotin-containing protein		
C;Keywords: biotin binding; seed		
F;125/Binding site: biotin (Lys)		
Query Match 51.4%; Score 54; DB 1; length 643; Best Local Similarity 52.2%; Pred. No. 47; Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0; Oy 2 XAEAAEKAKYAAEAAEKAKAX 24 Db 302 TAPVAAEKAKYTLQAAEKKSAG 324		
RESULT 28		
T34852		
probable secreted protein - Streptomyces coelicolor		
C;Species: Streptomyces coelicolor		
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004		
C;Accession: T34852		
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.		
submitted to the EMBL Data Library, February 1999		
A;Reference number: Z21559		
A;Accession: T34852		
A;Status: preliminary; Residues: 1-1156 <OLI>		
A;Cross-references: UNIPROT:Q9Z5A4; EMBL:AL035478; PIDN:CAM36606.1; GSPDB:GN00070; SCOP: C; Gene: SCOEDB; Superfamily: Escherichia coli ribosomal protein S2		
Query Match 51.4%; Score 54; DB 2; length 1156; Best Local Similarity 58.3%; Pred. No. 77; Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0; Oy 2 XAEAAEKAKYAAEAAEKAKAXA 25 Db 13 LAAMALALAATAAQAQAKAA 37		
RESULT 29		
A39638		
plectin - rat		
C;Species: Rattus norvegicus (Norway rat)		
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004		
C;Accession: A39638; S21876		
R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratowi		
J. Cell Biol. 114, 83-99, 1991		
A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with		
A;Reference number: A39638; MUID:91268156; PMID:2050743		
A;Accession: A39638		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-4687 <WIC>		
A;Cross-references: UNIPROT:P30427; EMBL:X9601; PIDN:G129885; PIDN:CAA42169.1; PID:9155		
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein; F;6-103/Domain: ribosomal protein S10 homology <RS10> F;184-399/Domain: alpha-actinin actin-binding domain homology <ACT>		
Query Match 51.4%; Score 54; DB 1; length 4687; Best Local Similarity 48.0%; Pred. No. 2.6e+02; Matches 12; Conservative 7; Mismatches 6; Indels 0; Gaps 0; Oy 1 AXAAEKAKYAAEAAEKAKAXA 25 Db 2221 SEAAEARRAAEAAEAREQAREAA 2245		
RESULT 30		
A05663		
antifreeze protein SS-8 - shorthorn sculpin		
C;Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)		
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004		
C;Accession: A05163		
R;Hew, C.L.; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.S.		
Eur. J. Biochem. 151, 167-172, 1985		
A;Title: Structures of shorthorn sculpin antifreeze polypeptides.		
A;Reference number: A91150; MUID:85285003; PMID:4029130		
A;Accession: A05163		
A;Molecule type: protein		
A;Residues: 1-45 <HEW>		
A;Cross-references: UNIPROT:P04368		
C;Superfamily: antifreeze; blocked amino end; plasma		
C;Keywords: antifreeze; blocked amino end; plasma		
F;9-45/Region: alanine-rich		
F;1/Modified site: blocked amino end (Met) #status experimental		
Query Match 51.0%; Score 53.5; DB 2; Length 45; Best Local Similarity 64.0%; Pred. No. 5.5; Matches 16; Conservative 3; Mismatches 5; Indels 1; Gaps 1; Oy 2 XAEAAEKAKYAAEAAEKAKAXA 25 Db 13 LAAMALALAATAAQAQAKAA 37		
RESULT 31		
S52118		
GTP-binding regulatory protein Gs alpha-XL chain - rat		
N;Alternative names: G protein XL-alpha-s		
C;Species: Rattus norvegicus (Norway rat)		
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 02-Feb-2001		
C;Accession: S52418		
R;Kehlenbach, R.H.; Matthey, J.; Huttner, W.B.		
Nature 372, 804-809, 1994		
A;Title: XL-alpha-s is a new type of G-protein.		
A;Reference number: S52418; MUID:9007273		

RESULT 32

Query Match 51.0%; Score 53.5; DB 2; Length 846;
Best Local Similarity 61.5%; Pred. No. 67;
Matches 16; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 AXAAEAKAKYAA-EAEKAKAYA 25
Db 170 AAAAAEPAEPAEPAEPAEPA 195

RESULT 33

Query Match 50.5%; Score 53; DB 2; Length 376;
Best Local Similarity 52.0%; Pred. No. 38;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAAEAKAKYAA-EAEKAKAYA 25
Db 177 AEAEAKAAEAKKAAEAKAA 201

RESULT 34

Query Match 50.5%; Score 53; DB 2; Length 386;
Best Local Similarity 59.1%; Pred. No. 39;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 BAERKAKYAA-EAEKAKAYA 25
Db 212 KAVEVAEKAADAEAKAA 233

RESULT 35

Query Match 50.5%; Score 53; DB 2; Length 386;
Best Local Similarity 59.1%; Pred. No. 39;
Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 4 BAERKAKYAA-EAEKAKAYA 25
Db 212 KAVEVAEKAADAEAKAA 233

RESULT 36

Query Match 50.5%; Score 53; DB 2; Length 205;
Best Local Similarity 52.0%; Pred. No. 23;
Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAAEAKAKYAA-EAEKAKAYA 25

A;Accession: T38147
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-893 <PEA>
 A;Cross-references: UNIPROT:O13898; EMBL:Z99295; PIDN:CCBL6577.1; GSPDB:GN00066; SPDB:SE
 A;Experimental source: strain 9721-; cosmid c22A12
 C;Genetics:
 A;Gene: SPDB:SPAC22A12.07c
 C;Superfamily: dolichyl-phosphate-mannose-protein mannosyltransferase
 Query Match 50 5%; Score 53; DB 2; Length 893;
 Best Local Similarity 48.0%; Pred. No. 80;
 Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 AXAAEAKAKYAAEAAKAKAKA 25
 Db 786 AEQEERAAEAKAASEAERSSSEA 810
 RESULT 37
 H8437 hypothetical protein PA1669 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C;Date: 15-Sep-2000 #sequence_revision 15-SEP-2000 #text_change 09-Jul-2004
 C;Accession: H83437
 R;Scover, C.K.; Pham, X.Q.; Erwin, A.L.; Micoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 L.; Lory, S.; Olson, M.V.
 Nature 405, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A;Reference number: A82950; MUID:2043737; PMID:10984043
 A;Accession: H83437
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:O91356; GB:AE004594; GB:AE004091; NID:99947630; PIDN:AAG0505
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA1669
 RESULT 38
 Query Match 50 0%; Score 52.5; DB 2; Length 1175;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 4; Mismatches 5; Indels 7; Gaps 1;
 Qy 1 AXAAEAKAKA-----KYAAEAKAKAKA 25
 Db 802 ALAEADKAKAKGKGKGAKAAAGKARDKA 833
 RESULT 39
 Query Match 49.5%; Score 52; DB 2; Length 147;
 Best Local Similarity 52.6%; Pred. No. 22;
 Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 XAAEAKAKYAAEAAKAKA 20
 Db 61 VAETARKSKKEFAEALSKA 79
 RESULT 40
 T26386 hypothetical protein Y105C5B.3 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T26386
 R;McMurray, A.
 submitted to the EMBL Data Library, September 1999
 A;Reference number: Z20208
 A;Accession: T26386
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-192 <WIL>
 A;Cross-references: UNIPROT:O9NAM6; EMBL:AL110479; NID:e1542153; PIDN:CAB54358.1; CESP:Y
 A;Experimental source: clone Y105C5B
 C;Genetics:
 A;Gene: CESP:Y105C5B.3
 C;Superfamily: human S-phase kinase-associated protein 1A
 Query Match 49.5%; Score 52; DB 2; Length 192;
 Best Local Similarity 70.6%; Pred. No. 28;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 EAEEAKAKYAAEAAKAKA 20
 Db 163 EAERAKAKAKA 179
 RESULT 41
 A25550 histone H1 - sea urchin (*Lytechinus pictus*)
 C;Species: *Lytechinus pictus* (painted urchin)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C;Accession: A25550

Qy 1 AXAAEAKAKYAAEAAKAKAKA 25
 Db 51 APAKAAAPAKTAAAPAKAAAPA 75
 RESULT 39
 D86389 hypothetical protein F28B23.4 - *Arabidopsis thaliana* (mouse-ear cress)
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: D86389
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso, C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzali, R.; Rooney, T.; Rowley, D.; Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venet, J.C.; Davis, R.W.; Ker, M.; Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*. A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: D86389
 A;Molecule type: DNA
 A;Residues: 1-147 <STO>
 A;Cross-references: UNIPROT:O9C674; GB:AE005172; NID:911079518; PIDN:AAG29229.1; GSPDB:G
 C;Genetics:
 A;Map position: 1
 Query Match 49.5%; Score 52; DB 2; Length 147;
 Best Local Similarity 52.6%; Pred. No. 22;
 Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 XAAEAKAKYAAEAAKAKA 20
 Db 61 VAETARKSKKEFAEALSKA 79
 RESULT 40
 T26386 hypothetical protein Y105C5B.3 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T26386
 R;McMurray, A.
 submitted to the EMBL Data Library, September 1999
 A;Reference number: Z20208
 A;Accession: T26386
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-192 <WIL>
 A;Cross-references: UNIPROT:O9NAM6; EMBL:AL110479; NID:e1542153; PIDN:CAB54358.1; CESP:Y
 A;Experimental source: clone Y105C5B
 C;Genetics:
 A;Gene: CESP:Y105C5B.3
 C;Superfamily: human S-phase kinase-associated protein 1A
 Query Match 49.5%; Score 52; DB 2; Length 192;
 Best Local Similarity 70.6%; Pred. No. 28;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 EAEEAKAKYAAEAAKAKA 20
 Db 163 EAERAKAKAKA 179
 RESULT 41
 A25550 histone H1 - sea urchin (*Lytechinus pictus*)
 C;Species: *Lytechinus pictus* (painted urchin)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C;Accession: A25550

R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone genes of the sea urchins *Lytechinus pictus* an
A;Reference number: A0550; MUID:87040778; PMID:3022245
A;Accession: A2550
A;Molecule type: DNA
A;Residues: 1-210 <KNO>
A;Cross-references: UNIPROT:P06144; GB:X04488; NID:99616; PIDN:CAA28177.1; PID:99617
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
Query Match 49.5%; Score 52; DB 2; Length 210;
Best local Similarity 52.0%; Pred. No. 30;
Matches 13; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
Qy 1 AXAAEAKKAYAAEAKAKAXA 25
Db 179 AKKAKKKPKAKKAKPKAKKPA 203

RESULT 42

HSUR1P
Histone H1, gonadal - sea urchin (*Parechinus angulosus*)
C;Species: *Parechinus angulosus* (angulate urchin)
C;Date: 31-Mar-1980 #sequence revision 31-Mar-1980 #text_change 09-Jul-2004
C;Accession: A91090; A91091; A02586
R;Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B.
Eur. J. Biochem. 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin *Parechinus angulosus* cyanogen bromide peptides.
A;Reference number: A91090; MUID:80156831; PMID:6767609
A;Comments: sequence of residues 1-84
A;Accession: A91090
A;Molecule type: protein
A;Residues: 1-248 <STR>
A;Cross-references: UNIPROT:P02256
R;Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Liebold, B.
Eur. J. Biochem. 104, 567-578, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin *Parechinus angulosus*
A;Reference number: A91091; MUID:80156832; PMID:7363905
A;Accession: A91091
A;Molecule type: protein
A;Residues: 80-248 <STR>
A;Note: 144-arg was also found
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleosome; sperm

Query Match 49.5%; Score 52; DB 1; Length 248;
Best local Similarity 54.2%; Pred. No. 35;
Matches 13; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Qy 2 XAAEAKKAYAAEAKAKAXA 25
Db 124 RTSAAKAKKAKKAALAKKAKKA 147

RESULT 43

S55219
ABA-inducible protein, landform-specific - *Riccia fluitans*
C;Species: *Riccia fluitans*
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S55219
R;Helliwege, E.M.; Dietz, K.J.; Hartung, W.
submitted to the EMBL Data Library, July 1995
A;Description: Abasic acid causes changes in gene expression involved in the induction
A;Reference number: S55619
A;Accession: S558219
A;Molecule type: mRNA
A;Residues: 1-288 <HEL>
A;Cross-references: UNIPROT:Q41154; EMBL:X89041; NID:9929818; PIDN:CAA61439.1; PID:9298

Query Match 49.5%; Score 52; DB 2; Length 288;
Best local Similarity 45.8%; Pred. No. 40;

Matches 11; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
Qy 2 XAAEAKKAYAAEAKAKAXA 25
Db 75 GAERKQAKNYGAKTEQAKSAAS 98

RESULT 44

S32234
transcription antitermination factor *nusG* - *Streptomyces griseus*
C;Species: *Streptomyces griseus*
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: S32234
R;Kuester, K.; Kuberski, S.; Pipersberg, W.; Distler, J.
submitted to the EMBL Data Library, March 1993
A;Description: Cloning and nucleotide sequence analysis of the *nusG-rplk-rplA-rplU-rplL* operon
A;Reference number: S32234
A;Accession: S32234
A;Molecule type: DNA
A;Residues: 1-294 <KUE>
A;Cross-references: UNIPROT:P36260; EMBL:Y72787; NID:9575399; PIDN:CAA51296.1; PID:960356
C;Genetics:
A;Gene: *nusG*
A;Start codon: GTG
C;Superfamily: transcription antitermination factor *nusG*
C;Keywords: transcription antitermination; transcription factor
Query Match 49.5%; Score 52; DB 2; Length 294;
Best local Similarity 61.9%; Pred. No. 40; 2; Mismatches 6; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 4 EAEEKAKYAAEAKAKAX 24
Db 212 EAEEKAAEAEAGKPAR 232

RESULT 45

S41061
probable transcription antitermination factor *nusG* - *Streptomyces griseus* (strain IFO1335)
C;Species: *Streptomyces griseus*
A;Variety: strain IFO1335
C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S41061
R;Miyake, K.; Onaka, H.; Horinouchi, S.; Beppu, T.
Biophys. Acta 1217, 97-100, 1994
A;Title: Organization and nucleotide sequence of the *secE-nusG* region of *Streptomyces griseus*
A;Reference number: S41059; MUID:94114580; PMID:8286423
A;Accession: S41059
A;Molecule type: DNA
A;Residues: 1-294 <MIY>
A;Cross-references: UNIPROT:P36260; EMBL:D17464; NID:9436786; PIDN:BAA04281.1; PID:948381
A;Experimental source: strain IFO13350
C;Genetics:
A;Gene: *nusG*
A;Start codon: GTG
C;Function:
A;Description: may be involved in antibiotics production
C;Superfamily: transcription antitermination factor *nusG*
Query Match 49.5%; Score 52; DB 2; Length 294;
Best local Similarity 61.9%; Pred. No. 40;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 4 EAEEKAKYAAEAKAKAX 24
Db 212 EAEEKAAEAEAGKPAR 232

Search completed: July 11, 2005, 09:47:10
Job time : 42 secs

9

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: July 11, 2005, 09:24:04 ; Search time 167 Seconds
(without alignment)
76.659 Million cell updates/sec

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

Result No.	Score	Query	Length	DB	ID	Description
1	71	67.6	485	2	Q8RXD0	Q8rx0 arabidopsis
2	71	67.6	924	2	Q9S108	Q9u08 arabidopsis
3	67	63.8	278	2	Q760M9	Q760m9 anophelles g
4	65	61.9	168	2	Q69307	Q69307 streptomyce
5	63	60.0	179	1	RL19AGR5	Q8ubz5 agrobacteri
6	63	60.0	413	2	Q83S1L	Q83s1l shigella fl
7	63	60.0	421	1	TOLECOLI	P19934 escherichia
8	63	60.0	421	2	Q8RTT1	Q8ft1 escherichia
9	61	58.1	441	2	Q6W8X8	Q6w8x8 rhodopseudo
10	61	58.1	593	2	Q8ZNE5	Q8zne5 salmoneilla
11	60.5	57.6	711	2	Q723F5	Q723f5 homo sapien
12	60.5	57.6	730	1	ELSHUMAN	P15502 homo sapien
13	60.5	57.6	757	2	Q14734	Q14734 homo sapien
14	60.5	57.6	757	2	Q75KU5	Q75mu5 homo sapien
15	60	57.1	105	2	Q6V503	Q6v503 rhodopseudo
16	60	57.1	177	2	Q9A865	Q9ab65 caulobacter
17	60	57.1	371	2	Q6M4V4	Q6m4v4 rhodopseudo
18	60	57.1	572	2	Q6Nh65	Q6nh65 corynebacte
19	60	57.1	738	2	Q6UuQ3	Q6uq3 chlamydomon
20	60	57.1	899	2	Q8N1Z0	Q8n1z0 neurospora
21	59.5	56.7	531	2	Q7PQ9	Q7pq9 anophelles g
22	59.5	56.7	647	2	Q891E4	Q891e4 bradyrhizob
23	59	56.2	347	2	Q9RKL9	Q9rl19 streptomyce
24	59	56.2	389	2	Q9CWT0	Q9cm70 pasteurella
25	59	56.2	1020	2	Q86PC3	Q86pc3 dirospohila
26	59	56.2	1020	2	Q9WJZ2	Q9wjz2 dirospohila
27	59	56.2	1069	2	Q86SG1	Q86sg1 dirospohila
28	59.5	55.7	181	2	Q64SR3	Q64sr3 bacteroides
29	58.5	55.7	496	2	Q8VQW6	Q8vqw6 azotobacter
30	58.5	55.7	508	2	Q9vgD2	Q9vgd2 dirospohila
31	58.5	55.7	664	2	Q9vgD3	Q9vgd3 dirospohila

ALIGNMENTS

Qry	1 AXAAEAKAAYAAEAAEAKAKAXA 25
Db	184 AAAGARDKAAKAAEAREKAKAA 208

RESULT 2

Qry	1 AXAAEAKAAYAAEAAEAKAKAXA 25
Db	184 AAAGARDKAAKAAEAREKAKAA 208

Query Match 67.6%; Score 71; DB 2; Length 485;
Best Local Similarity 68.0%; Pct. 2.1%; Mismatches 5; Indels 0; Gaps 0;

Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

DT 01-MAY-2000 (TREMBBLEL 13, Created)
DT 01-MAY-2000 (TREMBBLEL 13, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Auxilin-like protein.
 GN Name=T20K18.130; Synonyms=At4g12780;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCI_TaxID=3102;
 [1]

RP SEQUENCE FROM N.A.

RA sevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
 RA Bancroft I., Mewes H.W., Mayer K.F.X., Schnellier C.;
 RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;
 Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 [3]

RL SEQUENCE FROM N.A.
 RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL049640; CAB40951; -.
 DR EMBL; AL161554; CAB78320; 1; -.
 DR PIR; T0636; T0636.
 DR HSSP; Q27974; IN26.
 DR InterPro; IPR01623; DraJ_N.
 DR SMART; SM00271; DraJ_N.
 SQ SEQUENCE 924 AA; 102223 MW; 26E22C7C831EFF9B CRC64;
 Query Match 67.6%; Score 71; DB 2; Length 924;
 Best Local Similarity 68.0%; Pred. No. 3.5;
 Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 AXAAEAEKAAYAAEAKAKAKA 25
 Db 603 AAAGARDKAAKAAEAREKEKAA 627

RESULT 3

Q7Q0M9 PRELIMINARY; PRT; 278 AA.

AC Q7Q0M9;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE AGC8317 (Fragment).
 OS Name=agC054338; DBRNames=ENSAGG00000011932;

OC Anopheles gambiae str. PEST.
 Buharyota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 NCI_TaxID=180454;
 RN 11) SEQUENCE FROM N.A.

RC STRAIN=BST;

RA Anopheles Genome Sequencing Consortium;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Belongs to the ribosomal subunit L13 family.
 -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

EMBL; AA001008980; EAA14246; 1; -.

HSRP; 059300; 1J3A.
 GO:0015934; C:large ribosomal subunit; IEA.
 GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR005832; Ribosomal_L13.
 DR InterPro; IPR005755; Ribosomal_L13e/a.

PFam; PF00572; Ribosomal_L13; 1.

RESULT 4

O65907 PRELIMINARY; PRT; 168 AA.

ID 059907
 AC 065907;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Hypothetical protein SC05619.

GN ORFNnames=SC056135;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinomycetida; Streptomyctales;
 OC Streptomyceinae; Streptomyctaceae; Streptomyces.
 NCI_TaxID=1902;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;
 RX MEDLINE:21956410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chatterjee K.F., Cerdeno-Tarrazo A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Colling M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
 RA Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome" sequence of the model actinomycete Streptomyces
 coelicolor A3(2).
 RT Nature 417:41-47(2002).
 DR EMBL; AL939124; CRA19411; 1; -.
 DR PIR; T34804; T3404.
 DR PIR; T34804; T3404.
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 168 AA; 17934 MW; 72063B195040BDBE CRC64;
 Query Match 61.9%; Score 65; DB 2; Length 168;
 Best Local Similarity 62.5%; Pred. No. 4.4;
 Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AXAAEAEKAAYAAEAKAKAK 24
 Db 106 AEAKAAEKAERAJAAKAAAP 129

RESULT 5

R119_ASR75 STANDARD; PRT; 179 AA.

ID R119_ASR75
 AC Q8UBZ5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 23-OCT-2004 (Rel. 45, Last annotation update)

DE 50S ribosomal protein l19.

GN Name=RLPS; OrderedLocusNames=Atu2703; AGR_C 4900;
 OS Agrobacterium tumefaciens str C58 / ATCC 33970.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 NCI_TaxID=176299;
 RN [1]

RT	"The complete genome sequence of <i>Escherichia coli</i> K-12.,"
RT	Science 277:1453-1474 (1997).
[3]	
RP	SEQUENCE FROM N.A.
STRAIN=K12;	
MEDLINE=97061202; PubMed=8905232;	
RA	Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA	Ikenoto K., Inda T., Itou T., Kajimura M., Kanai K., Kashimoto K.,
RA	Kimura S., Kigawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA	Mori H., Motoura K., Nakamura Y., Nasimoto H., Nishio Y., Saito N.,
RA	Sampei G., Seki Y., Tagami H., Takekoto K., Wada C., Yamamoto Y.,
RA	Yano M., Horinouchi T.,
RT	"A 718-kb DNA sequence of the <i>Escherichia coli</i> K-12 genome
RT	corresponding to the 12.7-28.0 min region on the linkage map.,"
RL	DNA Res. 3:137-155(1996).
[4]	
RN	DOMAINS.
RX	MEDLINE=91296736; PubMed=2068069;
RA	Levengood S.K., Beyer W.F. Jr., Webster R.E.;
RT	"TolA, a membrane protein involved in colicin uptake contains an extended helical region.,"
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943 (1991).
[5]	
RN	INTERACTION WITH PORINS.
RX	MEDLINE=91133211; PubMed=8978668;
RA	Dericiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,
RT	"TolA central domain interacts with <i>Escherichia coli</i> porins.,"
RL	EMBL; J. 15:6408-6415(1996).
[6]	
RX	X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 298-421.
RA	MEDLINE=93132679; PubMed=1040600; DOI=10.1016/S0959-2126(99)80092-6;
RA	Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
RT	"Filamentous phage infection: crystal structure of g3p in complex with its coreceptor, the C-terminal domain of TolA.,"
RL	Structure 7:711-722(1999).
CC	-!- FUNCTION: Involved in the tonB-independent uptake of group A colicins (colicins A, E1, E2, E3, and K). Necessary for the colicins to reach their respective targets after initial binding to the bacteria. Also involved in the translocation of bacteriophage DNA.
CC	-!- SUBUNIT: Interacts, via domain II, with porins ompC, phoE and lamB.
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	
DR	EMBL; M2832; AAA24683.1; -.
DR	EMBL; U00096; AAC73833.1; -.
DR	EMBL; D0013; BAA35405.1; -.
DR	PIR; JVV0057; JVV0057.
PDB	1TOL; X-RAY; A=-.
DR	EchoBASE; EB1000; -.
DR	EcoGene; EG11007; tolA.
DR	InterPro; IPR010528; TolA.
KW	PFam; PF06519; TolA. 3D-structure; Bacteriocin transport; Complete proteome; Inner membrane; Protein transport; Repeat; Transmembrane; Transport.
FT	DOMAIN 1 35 421 Cytoplasmic (Potential). TRANSMEM 14 34 Periplasmic (Potential). DOMAIN 1 13 34 Cytoplasmic (Potential). DOMAIN 35 421 Domain II (alpha-helical). DOMAIN 311 421 Domain III (functional). DOMAIN 224 292 13 X tandem repeats of [EDA]-K(1,2) - A(2,4).
FT	REPEAT 224 229 1.
REPEAT	224 229 1.
FT	REPEAT 230 235 3.
FT	REPEAT 240 245 4.
FT	REPEAT 244 246 5.
FT	REPEAT 250 255 6.
FT	REPEAT 256 260 7.
FT	REPEAT 261 266 8.
FT	REPEAT 267 271 9.
FT	REPEAT 272 277 10.
FT	REPEAT 278 282 11.
FT	REPEAT 283 287 12.
FT	REPEAT 288 292 13.
FT	DISTRIFID 363 388 388
FT	HELIX 335 349 349
FT	TURN 350 351 351
FT	TURN 353 354 354
FT	HELIX 355 358 358
FT	TURN 359 360 360
FT	STRAND 363 369 369
FT	TURN 371 372 372
FT	STRAND 375 383 383
FT	HELIX 385 397 397
FT	HELIX 406 412 412
FT	TURN 413 414 414
FT	STRAND 416 421 421
FT	SEQUENCE 421 AA; 43156 MW; 882F52B4B97C655E CRC64;
QY	Query Match 60.0%; Score 63; DB 1; length 421;
Db	Best Local Similarity 60.0%; Pred. No. 16; Mismatches 6; Mismatches 15; Conservative 15; Gaps 0; Gaps 0;
QY	1 AKAKAAEKAKYAAEAKKAKA 25 151 ADAKAAEAKKAADAKKGAEEA 175
RESULT 8	
Q8FUT1	PRELIMINARY; PRT; 421 AA.
ID	Q8FUT1;
AC	Q8FUT1; (TREMBIrel. 23, Created)
DT	01-MAR-2003 (TREMBIrel. 23, Last sequence update)
DT	01-MAR-2004 (TREMBIrel. 26, Last annotation update)
DB	TOL protein.
GN	Name=tolA; Order=locusName=cc0818;
OS	Escherichia coli O6.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
OX	NCBI_TaxID=217992;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=O6:HL / CFT073 / ATCC 700928;
RX	MEDLINE=2238234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA	Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles B.L., Liou S.-R., Böttin A., Hackett J., Stroud D.,
RA	Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA	Mobley H.L.T., Donnenberg M.S., Blattner F.R.,
RT	"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic <i>Escherichia coli</i> ,"
RT	of <i>Escherichia coli</i> K12.,"
RL	Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR	EMBL; AEG1675; AAM79291.1; -.
DR	HSSP; P19934; 1TOL.
DR	InterPro; IPR01058; TolA.
DR	PFam; PF06519; TolA. 1.
KW	Complete proteome.
SQ	SEQUENCE 421 AA; 43184 MW; DB296626P056D385 CRC64;
QY	Query Match 60.0%; Score 63; DB 2; length 421;
Db	Best Local Similarity 60.0%; Pred. No. 16; Mismatches 6; Mismatches 15; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 151 ADAKAEEAKKAADAKKKAAEA 175
 RESULT 9
 ID Q6N8X8 PRELIMINARY; PRT; 441 AA.
 ID Q6N8X8 (TREMBrel. 27, Created)
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)
 DB OmpA/MotB domain, possible porin precursor.
 GN OrderidococcusNames:RPA174;
 OS Rhodopseudomonas palustris.
 OC Bacteriia; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OK NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCUG009 / ATCC BAA-98;
 RX PubMed=4704707; DOI=10.1038/nbt923;
 RA Larimer S.W., Chain P., Hauser L., Lamerdin J.B., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.I., Lang A.S., Tahita P.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres Y, Torres J.L., Perea C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 photosynthetic bacterium Rhodopseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004);
 CC -i- SIMILARITY: Belongs to the OmpA family.
 DR EMBL; BX572598; CAB27215.1; -.
 DR GO; GO:0016021; C:outer membrane (Bensu Gram-negative Bacteria); IEA.
 DR GO; GO:0009279; C:outer membrane (Bensu Gram-negative Bacteria); IEA.
 DR PROTO; PDB00330; OMPA/MotB; 1.
 DR InterPro; IPR006654; Bac_OmpA.
 DR Pfam; PF00691; OmpA; 1.
 DR InterPro; IPR01021; OMP DOMAIN.
 DR InterPro; IPR006665; OMP/MotB.
 DR PRTS; PR01021; OMP DOMAIN.
 DR PROTO; PDB00330; OMPA/MotB; 1.
 KW Complete proteome; Porin; Signal.
 FT SIGNAL 1 27 Potential.
 SQ SEQUENCE 441 AA; 4811 MW; F5BB66A4AEE183A0 CRC64;
 Query Match 58.1%; Score 61; DB 2; Length 441;
 Best Local Similarity 62.5%; Pred. No. 28;
 Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AXAAEAKAKYAAEAKAKAK 24
 Db 237 ADSEKEAAAKAAEAKAKAA 260
 RESULT 10
 Q8ZN85 PRELIMINARY; PRT; 593 AA.
 AC Q8ZN85;
 AC Q8ZN85; (TREMBrel. 20, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 26, Last annotation update)
 DE Putative von Willebrand factor, vWF type A domain.
 GN Name=yfbk; OrderidococcusNames:STM315;
 OS *Salmonella* *typhimurium*; *Salmonella*; *Proteobacteria*; *Enterobacteriales*; *Enterobactericeae*; *Salmonellae*.
 OC NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J27;
 RX MEDLINE=21534948; PubMed=1167609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwoll S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvane E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoenkking T., Nhan M.,
 RA Waterston R., Wilson R.K., "Complete genome sequence of *Salmonella enterica* serovar *Typhimurium*

RT LT2.;"
 RL Nature 413:852-856(2001).
 DR EMBL; AS008803; AA121216.1; -.
 DR Pfam; PF00092; VWA; 1.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS50234; VWEA; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 593 AA; 64640 MW; 595CA58158968357 CRC64;
 Query Match 58.1%; Score 61; DB 2; Length 593;
 Best Local Similarity 62.5%; Pred. No. 35;
 Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 2 XAEAEAKAKYAAEAKAKAXA 25
 Db 57 QAEAQOAKAKAABYAEAKALADA 80

RESULT 11
 Q7Z3F5 PRELIMINARY; PRT; 711 AA.
 ID Q7Z3F5
 AC Q7Z3F5; (TREMBrel. 25, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DR DE HYPOTHETICAL PROTEIN DKRZP86F06102;
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human fetal kidney;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Meves H.W., Weil B., Anid C., Osanger A., Bobo G., Han M., Wiemann S.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537939; CAD97910.1; -.
 DR InterPro; IPR001451; DR, Hexapep_transf.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 711 AA; 61765 MW; 95B62A99BA4989B CRC64;
 Query Match 57.6%; Score 60.5; DB 2; Length 711;
 Best Local Similarity 58.6%; Pred. No. 47;
 Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;
 QY 1 AXAAEAKAKY---AEEAKAKAK 24
 Db 446 AQAAAAKAKAKYGVGTPAAAKAKAA 474

RESULT 12
 EBL_HUMAN STANDARD; PRT; 730 AA.
 ID EBL_HUMAN
 AC P1502; Q14233; Q14238;
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Elastin precursor (Tropoelastin).
 GN Name=ELN;
 OS Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RX MEDLINE=87289668; PubMed=3039501;
 RA Indik Z., Yeh H., Ornsstein N., Sheppard P., Anderson N.,
 RA Rosenblom J.C., Peltonen L., Rosenblom J.; Rosenblom J.,
 RT "Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA.;"
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987);
 RL

RN [2] SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE:Skin fibroblast;
 RC MEDLINE:89009960; PubMed=3171221;
 RA Fazio M.J., Olsen D.R., Kaup B.A., Baldwin C.T., Indik Z.,
 RA Ornstein-Goldstein N., Yeh H., Rosenblum J., Utton J.;
 RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
 RT recombinant cDNA library: further elucidation of alternative splicing
 RT utilizing exon-specific oligonucleotides.;"
 RL J. Invest. Dermatol. 91:458-464(1988).
 RN [3] SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
 RP TISSUE:Placenta;
 RX MEDLINE:80156138; PubMed=2831431;
 RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
 RA Rosenblum J., Utton J.;
 RT "Isolation and characterization of human elastin cDNAs, and age-
 RT associated variation in elastin gene expression in cultured skin
 RT fibroblasts.;"
 RL Lab. Invest. 58:270-277(1988).
 RN [4] SEQUENCE OF 603-730 FROM N.A.
 RP TISSUE:Hipocampus and Placenta;
 RX MEDLINE:96291399; PubMed=869688; DOI=10.1016/S0092-8674(00)80077-X;
 RA Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
 RA Robinson B.P., Klein B.P., Ensing G.J., Everett L.A., Green B.D.,
 RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
 RA Keating M.T.;
 RT "LIM-kinase hemiagyosity implicated in impaired visuospatial
 RT constructive cognition.;"
 RL Cell 86:59-69(1996).
 RN [5] INVOLVEMENT IN CUTIS LAXA.
 RX MEDLINE:99091639; PubMed=9873040; DOI=10.1074/jbc.274.2.981;
 RA Zhang M.-C., He L., Giro M., Yong S.J., Tiller G.E., Davidson J.M.;
 RT "Cutis laxa arising from frameshift mutations in exon 30 of the
 RT elastin gene (ELN).;"
 RL J. Biol. Chem. 274:981-986(1999).
 RN [6] INVOLVEMENT IN SVAS.
 RP INVOLVEMENT IN SVAS.
 RX PubMed=10942104;
 RA Urban Z., Michelis V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
 RA Munich A., Syskens B., Gewillig M., Bevrriadt K., Boyd C.D.;
 RT "Isolated supravalvular aortic stenosis: functional haploinsufficiency
 of the elastin gene as a result of nonsense-mediated decay.;"
 RL Hum. Genet. 106:577-588(2000).
 CC !- FUNCTION: Major structural protein of tissues such as aorta and
 CC nuchal ligament, which must expand rapidly and recover completely.
 CC !- SUBUNIT: The polymeric elastin chains are cross-linked together
 CC into an extensible 3D network.
 CC !- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
 CC !- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=?;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P15502-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P15502-2; Sequence=VSP 004243;
 CC !- PTM: The crosslinks are made of deaminated lys.
 CC !- DISEASE: Defects in ELN are a cause of autosomal dominant cutis
 CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder
 CC characterized by loose, hyperextensible skin with decreased
 CC resilience and elasticity leading to a premature aged appearance.
 CC The skin changes are often accompanied by extracutaneous
 CC manifestations, including pulmonary emphysema, bladder
 CC diverticula, pulmonary artery stenosis and pyloric stenosis.
 CC !- DISEASE: Haploinsufficiency of ELN may be the cause of certain
 CC cardiovascular and musculo-skeletal abnormalities observed in
 CC Williams-Bauren syndrome (WBS) [MIM:194050]. WBS is a rare
 CC developmental disorder and a contiguous gene deletion syndrome
 CC involving genes from chromosome band 7q11.23.
 CC !- DISEASE: Defects in ELN are the cause of supravalvular aortic
 CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of

CC the ascending aorta which can occur sporadically, as an autosomal
 CC dominant condition, or as one component of Williams-Bauren
 CC syndrome.

CC -----

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CC -----

CC DR EMBL: M17282; AAC98394.1; --.
 CC DR EMBL: M16937; AAC98394.1; JOINED.
 CC DR EMBL: M17265; AAC98394.1; JOINED.
 CC DR EMBL: M17266; AAC98394.1; JOINED.
 CC DR EMBL: M17277; AAC98394.1; JOINED.
 CC DR EMBL: M17268; AAC98394.1; JOINED.
 CC DR EMBL: M17270; AAC98394.1; JOINED.
 CC DR EMBL: M17271; AAC98394.1; JOINED.
 CC DR EMBL: M17272; AAC98394.1; JOINED.
 CC DR EMBL: M17273; AAC98394.1; JOINED.
 CC DR EMBL: M17275; AAC98394.1; JOINED.
 CC DR EMBL: M17276; AAC98394.1; JOINED.
 CC DR EMBL: M17277; AAC98394.1; JOINED.
 CC DR EMBL: M17278; AAC98394.1; JOINED.
 CC DR EMBL: M17279; AAC98394.1; JOINED.
 CC DR EMBL: M17280; AAC98394.1; JOINED.
 CC DR EMBL: M17281; AAC98394.1; JOINED.
 CC DR EMBL: M17282; AAC98394.1; JOINED.
 CC DR EMBL: M24782; AAC53190.1; --.
 CC DR EMBL: M6292; AAC17544.1; --.
 CC DR EMBL: X15603; CAA33627.1; --.
 CC DR PIR: A22707; EAHU.
 CC DR HSSP; P50099; 1ZEU.
 CC DR Genew; HGNC:3327; ELN.
 CC DR MIM; 132700; --.
 CC DR MIM; 132700; --.
 CC DR MIM; 134050; --.
 CC DR MIM; 134050; --.
 CC DR GO; GO:0005500; --.
 CC DR GO; GO:0005578; C:extracellular matrix; TAS.
 CC DR GO; GO:0005615; C:extracellular space; TAS.
 CC DR GO; GO:0008283; P:cell proliferation; TAS.
 CC DR GO; GO:0008015; P:circulation; TAS.
 CC DR GO; GO:0009887; P:organogenesis; TAS.
 CC DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.
 CC DR InterPro; IPR003919; tropoelastin.
 CC DR PRINTS; PR01500; TROPBLASTIN.
 CC DR Alternative splicing; Repeat; Signal; Structural protein;
 CC KW Williams-Bauren syndrome.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 730 Elastin
 CC FT DISULFID 720 725 By similarity.
 CC FT VARSPLIC 472 477 Missing (in Isoform 2).
 CC FT /FTId=SP 004243;
 SQ SEQUENCE 730 AA; 63260 MW; AB06D15BAS67AB46 CRC64;

Query Match 57.6%; Score 60.5%; DB 1; Length 730;
 Best Local Similarity 58.6%; Pred. No. 48; Mismatches 4; Indels 5; Gaps 1;
 Matches 17; Conservative 3; MisMatches 4; Indels 5; Gaps 1;

QY 1 AXAABAEKAKY---AEEAEKAKAKX 24
 Db 441 AQAAGAAKAKYVGTPAAAKAKA 469

RESLT 13
 Q14234
 ID Q14234
 AC Q14234;
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)

DT 01-MAR-2004. (TREMBrel. 26, last annotation update)
 DE Elastin;
 GN Name=ELN;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87289668; PubMed=3039501;
 RX "Alternative splicing of human elastin mRNA indicated by sequence analysis of cloned genomic and complementary DNA.";
 RT Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N., Rosenblom J.C., Petronen L., Rosenblom J.,
 RA "Structure of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87274506; PubMed=3038460;
 RA Indik Z., Yoon K., Morrow S.D., Cicilia G., Rosenblom J., Rosenblom J., Ornstein-Goldstein N.;
 RA "Structure of the human elastin gene: great abundance of Alu repetitive sequences and few coding sequences.";
 RT Connect. Tissue Res. 161:197-211(1987).
 RL EMBL; MI:7282; AAC93951;
 DR EMBL; MI:6983; AAC93951; JOINED.
 DR EMBL; MI:7265; AAC93951; JOINED.
 DR EMBL; MI:7266; AAC93951; JOINED.
 DR EMBL; MI:7267; AAC93951; JOINED.
 DR EMBL; MI:7268; AAC93951; JOINED.
 DR EMBL; MI:7270; AAC93951; JOINED.
 DR EMBL; MI:7271; AAC93951; JOINED.
 DR EMBL; MI:7272; AAC93951; JOINED.
 DR EMBL; MI:7273; AAC93951; JOINED.
 DR EMBL; MI:7274; AAC93951; JOINED.
 DR EMBL; MI:7275; AAC93951; JOINED.
 DR EMBL; MI:7276; AAC93951; JOINED.
 DR EMBL; MI:7277; AAC93951; JOINED.
 DR EMBL; MI:7278; AAC93951; JOINED.
 DR EMBL; MI:7279; AAC93951; JOINED.
 DR EMBL; MI:2880; AAC93951; JOINED.
 DR EMBL; MI:17281; AAC93951; JOINED.
 DR GO; GO:0005579; C:extracellular matrix (sensu Metazoa); IFA;
 DR GO; GO:0030023; F:extracellular matrix constituent conferring . . .; IFA.
 DR InterPro; IPR01451; Hexapep transf.
 DR InterPro; IPR03979; tropoelastin.
 DR PRINTS; PR01500; TROPOLASTIN.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
 DR SEQUENCE 757 AA; 66136 MW; 2B24F955D8360738 CRC64;
 Query Match 57.6%; Score 60.5%; DB 2; Length 757;
 Best Local Similarity 58.6%; Pred. No. 49;
 Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;
 Qy 1 AXAEEAKAKY----AEEAEKAKAX 24
 Db 441 AQAAGAAKAKAKVGVGTAAAKAKAA 469
 RESULT 14
 ID 075M05
 AC 075M05
 DT 05-JUL-2004 (TREMBrel. 27, Created)
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)
 DR Hypothetical protein ELN.
 GN Name=ELN;
 OS Homo sapiens (Human);
 OC Bacteria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22737999; PubMed=12053949; DOI=10.1038/nature01782;
 RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
 RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
 RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
 RA Fewell G.A., Delhaunty K.D., Miner T.L., Nash W.E., Cordeiro M., Du H.,
 RA Sun H., Edwards J., Bridgshav-Cordrum H., Ali J., Andrews S., Isak A.,
 RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
 RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
 RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlbberg S.,
 RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
 RA Tin-Wilam A.M., Abbott A., Minx P., Maupin R., Stromatt C.,
 RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
 RA Wendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
 RA Bieri T.A., Nelson J.O., Berrowicz N., Wohltmann P.E., Cook L.L.,
 RA Hickernbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
 RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,
 RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Babb K.,
 RA Simms E., Levy R., Cleland J., Kaul R., Kent W.J., Furey T.S.,
 RA Baertsch R.A., Brent M.R., Keibler E., Flieck P., Bork P., Suyama M.,
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
 RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
 RA Waterston R.H., Wilson R.K.;
 RT "The DNA sequence of human chromosome 7.";
 RT Nature 424:157-164(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RN Watson R.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Wilson R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC005056; ASN07435.1;
 DR GO; GO:0005578; C:extracellular matrix structural constituent; IFA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IFA.
 DR InterPro; IPR01451; Hexapep transf.
 DR InterPro; IPR03979; tropoelastin.
 DR PRINTS; PR01500; TROPOLASTIN.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
 KW Hypothetical protein.
 DR SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
 Query Match 57.6%; Score 60.5%; DB 2; Length 757;
 Best Local Similarity 58.6%; Pred. No. 49;
 Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;
 Qy 1 AXAEEAKAKY----AEEAEKAKAX 24
 Db 441 AQAAGAAKAKAKVGVGTAAAKAKAA 469
 RESULT 15
 ID 06N503
 AC 06N503
 DT 05-JUL-2004 (TREMBrel. 27, Created)
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)
 DR Hypothetical protein.
 GN OrderedLocusName=RP3190;
 OS Rhodopseudomonas palustris;
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CGA009 / ATCC BAA-98;
 RX Published=1474077; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauber L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelleter D.A., Beatty J.T., Lang A.S., Tanita P.R.,
 RA Gibson J.L., Hanson T.B., Bobst C., Torres Y, Torres J.L., Perea C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile

RT photosynthetic bacterium *Rhodopseudomonas palustris*.";
 RL Nat. Biotechnol. 22:55-61 (2004).
 DR EMBL; BX572603; CAB28621.1; -.
 DR GO; GO:0007936; C: nucleosome; IEA.
 DR GO; GO:005634; C: nucleus; IEA.
 DR GO; GO:0006377; F: DNA binding; IEA.
 DR GO; GO:0006334; P: nucleosome assembly; IEA.
 DR InterPro; IPR005819; Histone_H5.
 DR PRINTS; PR00624; HISTONH5.
 DR Complete proteome; Hypothetical protein.
 KW SEQUENCE 105 AA; 11042 MW; CEDB59B3D937B980 CRC64;
 SQ

Query Match 57.1%; Score 60; DB 2; Length 105;
 Best Local Similarity 56.0%; Pred. No. 11;
 Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 AXAAEAEKAAYAEEAAEAKAKAXA 25
 Dr 58 AAKAKAKKAAKKAKPKAKAKAA 82

RESULT 16

Q9AB65 PRELIMINARY; PRT; 177 AA.
 AC Q9AB65;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE ATP synthase F0, B' subunit.
 GN OrderdlocusNames=CC0366;
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / ATCC BAA-98;
 RX Published=1470470; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Haaser L., Lamerdin J.F., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.R., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres Y, Torres J.L., Perea C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 photosynthetic bacterium *Rhodopseudomonas palustris*";
 RL Nat. Biotechnol. 22:55-61 (2004).
 CC -1- FUNCTION: This small ubiquitous enzyme is essential for
 CC maintenance and cell growth (By similarity).
 CC -1- CATALYTIC ACTIVITY: ADP + AMP = 2 ADP.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the adenylylate kinase family.
 DR EMBL; BX572603; CAB28670.1; -.
 DR HSSP; P05082; IAK3.
 DR GO; GO:0004017; F: adenylylate kinase activity; IEA.
 DR GO; GO:0005524; F: AMP binding; IEA.
 DR GO; GO:0016301; F: kinase activity; IEA.
 DR GO; GO:0016740; F: transferase activity; IEA.
 DR InterPro; IPR006850; Adenylylate_kin.
 DR InterPro; IPR006259; Adenylyl_kin_sub.
 DR Pfam; PF00405; ADK; 1.
 DR PRINTS; PR00094; ADENYLKINASE.
 DR PRODOM; PD000657; Adenylylate_kin; 1.
 DR TIGRMS; TIGR01351; adk; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 DR ATP-binding; Complete proteome; Kinase; Transferase.
 KW SEQUENCE 371 AA; 37905 MW; 9BB86A147A346205 CRC64;
 SQ

Query Match 57.1%; Score 60; DB 2; Length 371;
 Best Local Similarity 56.0%; Pred. No. 32;
 Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 AXAAEAEKAAYAEEAAEAKAKAXA 25
 Dr 306 AVAKAGKKAAKAATKAAGAKPTA 330

RESULT 18

Q6NH65 PRELIMINARY; PRT; 572 AA.
 AC Q6NH65;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Putative invasion protein.
 GN OrderdlocusNames=BP1281;
 OS Corynebacterium diphtheriae.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1717;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Biotype Gravis / NCTC 13129;
 RX PubMed=22965443; DOI=10.1093/nar/gkg874;
 RA Cedeno-Tarrega A.-M., Efstatiou A., Dover L.G., Holden M.T.G.,
 Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
 RESULT 17

RA De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T., [2]
 RA Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
 RA Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
 RA Whitehead S., Barrell B.G., Parkhill J.;
 RT "The complete genome sequence and analysis of *Corynebacterium*
 RT *diphtheriae* NCTC1129.";
 RL Nucleic Acids Res. 31:516-523 (2003).
 DR EMBL; BX248357; CAB49808.1; -.
 DR InterPro; IPR00064; NLP_P60.
 DR Pfam; PF00877; NLPC_P60; 1.
 KW Complete proteome.
 SQ SEQUENCE 572 AA; 61149 MW; 6ECE6CD145263F2 CRC64;
 Query Match 57.1%; Score 60; DB 2; Length 572;
 Best Local Similarity 56.0%; Pred. No. 45;
 Matches 14; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AXAENAEKAKYAAEAEKA
 DB 294 AARKAKKEEARIAAEAKAKA
 SEQUENCE 318 AA; 95309 MW; 5A10C4AC09D8F9 CRC64;
 RESULT 19
 ID 06UBQ3 PRELIMINARY; PRT; 738 AA.
 AC 06UBQ3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Radial spoke protein 2.
 OS *Chlamydomonas reinhardtii*.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC *Chlamydomonadaceae*; *Chlamydomonas*.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang P., Yang C., Sale W.S.;
 RT "Flagellar radial spoke protein 2 is a calmodulin binding protein
 required for motility in *Chlamydomonas reinhardtii*.";
 RL Eukaryotic Cell 3:72-81 (2004).
 DR EVO37263; AA092371.1; -.
 DR InterPro; IPR007858; DPF-30.
 DR Pfam; PF05186; DPY-30; 1.
 SQ SEQUENCE 738 AA; 77362 MW; 506811B4975539AD CRC64;
 Query Match 57.1%; Score 60; DB 2; Length 738;
 Best Local Similarity 62.5%; Pred. No. 55;
 Matches 15; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 2 XAEAEKA
 DB 651 AAAAEAAAEEAEAAAEEAAA 674
 RESULT 20
 ID QBNIZO PRELIMINARY; PRT; 899 AA.
 AC QBNIZO;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Related to kinetoplast-associated protein Kap.
 GN Name=SF3-190;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 RN [1] - TaxID=5141;
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nykatura G., Mewes H.W., Mainihaup G.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

RESULT 21
 ID QTPNQ9 PRELIMINARY; PRT; 531 AA.
 AC QTPNQ9;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DE ENSANGP0000017612 (Fragment).
 GN Name=ENSANGG0000015123;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OC NCBI_TaxID=10454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=EST;
 RC Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RL Anopheles Genome Sequencing Consortium;
 CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR HSSP; P04802; IASZ.
 DR GO; GO:0005377; C-cytoplasm; IEA.
 DR GO; GO:0004815; F-aspartate-tRNA ligase activity; IEA.
 DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0003676; F-nucleic acid binding; IEA.
 DR GO; GO:0006422; F-aspartyl-tRNA aminoacylation; IEA.
 DR InterPro; IPR004523; tRNA arch.
 DR InterPro; IPR00894; Nucleic acid OB.
 DR InterPro; IPR04364; tRNA-synt_2.
 DR InterPro; IPR02312; tRNA-synt.asp.
 DR InterPro; IPR00465; tRNA anti.
 DR InterPro; IPR00695; tRNA_ligase_II.
 DR Pfam; PF00152; tRNA-synt_2; 1.
 DR Pfam; PF01336; tRNA_anti; 1.
 DR PRINTS; PRO142; tRNA-synt.asp.
 DR TIGRFAMs; TIGR00058; asPS arch; 1.
 DR PROSITE; PS50862; AA_tRNA_LIGASE_II; 1.
 SQ SEQUENCE 531 AA; 58958 MW; A9468D3F53448317 CRC64;
 Query Match 56.7%; Score 59.5; DB 2; Length 531;
 Best Local Similarity 69.6%; Pred. No. 48;
 Matches 16; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
 QY 1 AXAENA
 DB 1 AGABATSKGAKKAKDAAKA 23
 RESULT 22
 ID Q89IE4 PRELIMINARY; PRT; 647 AA.
 AC Q89IE4;

DT 01-JUN-2003 (TREMBrel. 24, Created)
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE BL15695 protein.
 GN *Orderobactismates-bl15695;*
 OS *Bradyrhizobium japonicum.*
 OC *Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;*
 OC *Bradyrhizobiaceae; Bradyrhizobium.*
 NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE:22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamiawa K., Uchiimi T.,
 RA Sasamoto S., Watanabe A., Idezawa K., Iriuchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpou S., Tsuruoka H., Wada T., Yamada M.,
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT *Bradyrhizobium japonicum USDA110.*";
 RL DNA Res. 9:89-197 (2002).
 DR EMBL; AR005935; BAC5960.1; -.
 GO; GO:003063; *Protease activity; IBA.*
 GO; GO:006508; *Proteolysis and peptidolysis; IBA.*
 DR InterPro; IPR001309; ICB_p20.
 DR PROSITE; PS0208; *CASPASE_P20; -1.*
 KW PROSITE; PS0208; *CASPASE_P20; -1.*
 SQ SEQUENCE 647 AA; 69607 MW; 69FB4EDECFCF836 CRC64;
 Query Match 56.7%; Score 59.5; DB 2; Length 647;
 Best local Similarity 53.3%; Pred. No. 57;
 Matches 16; Conservative 5; Mismatches 4; Indels 5; Gaps 1;
 QY 1 AXAERAEEK---AAXYAAEAEEKAKAXA 25
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DR Probable peptidase.
 ORName=SCD17.12;
 OS *Streptomyces coelicolor.*
 OC *Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;*
 OC *Streptomyces; Streptomyces; Streptomyces.*
 NCBI_TaxID=902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2) / M145;
 RX MEDLINE=21995410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Taronga A.-M., Challis G.L.,
 RA Thomson N.R., James D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larkie L., Ridgway J., Oliver K., O'Neill S.,
 RA Rabinowitz B., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squires R., Squires S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2).";
 RL Nature 417:141-147 (2002).
 DR EMBL; AL939118; CAB5369.1; -.
 GO; GO:004222; *F-metalloendopeptidase activity; IBA.*
 GO; GO:006508; *Proteolysis and peptidolysis; IBA.*
 DR InterPro; IPR002806; *Peptidase_M23.*
 DR InterPro; IPR011054; *Rudmnt_hyb_motif.*
 DR Pfam; PF01551; *Peptidase_M23; 1.*
 Complete proteome.

RESULT 23
 Q9RKL9 PRELIMINARY; PRT; 347 AA.
 ID Q9RKL9
 AC Q9RKL9;
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DR Probable peptidase.
 ORName=SCD17.12;
 OS *Streptomyces coelicolor.*
 OC *Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;*
 OC *Streptomyces; Streptomyctaceae; Streptomyces.*
 NCBI_TaxID=902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2) / M145;
 RX MEDLINE=21995410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Taronga A.-M., Challis G.L.,
 RA Thomson N.R., James D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larkie L., Ridgway J., Oliver K., O'Neill S.,
 RA Rabinowitz B., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squires R., Squires S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2).";
 RL Nature 417:141-147 (2002).
 DR EMBL; AL939118; CAB5369.1; -.
 GO; GO:004222; *F-metalloendopeptidase activity; IBA.*
 GO; GO:006508; *Proteolysis and peptidolysis; IBA.*
 DR InterPro; IPR002806; *Peptidase_M23.*
 DR InterPro; IPR011054; *Rudmnt_hyb_motif.*
 DR Pfam; PF01551; *Peptidase_M23; 1.*
 Complete proteome.

RESULT 24
 Q9CWT0 PRELIMINARY; PRT; 389 AA.
 ID Q9CWT0
 AC Q9CWT0;
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE TOLA.
 Name=tOLA; OrderedLocusNames=PM0968;
 OS *Peptococcaceae; Pasteurellales.*
 OC *Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;*
 OC *Pasteurellaceae; Pasteurellla.*
 NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RX MEDLINE:2115866; PubMed=1248100; DOI=10.1073/pnas.051634598;
 RA May B.-J., Zhang Q., Li L.-L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of *Pasteurellla multocida* Pm70.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
 DR EMBL; AR006136; AAC03052.1; -.
 HSSP; P01096; IGM2.
 DR InterPro; IPR009148; Siba.
 DR InterPro; IPR010528; TOLA.
 DR InterPro; IPR000333; Tropomyosin.
 DR Pfan; PP06519; TOLA; 1.
 DR PRINTS; PR01852; SIBAPROTEIN.
 DR PRINTS; PR00194; TROPOMOSIN.
 KW Complete proteome.
 SQ SEQUENCE 389 AA; 42197 MW; B4032F2A2FD9E943 CRC64;
 Query Match 56.2%; Score 59; DB 2; Length 389;
 Best local Similarity 60.0%; Pred. No. 43;
 Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AXAFARAKAKYAAEAKAKAKAXA 25
 DB 2.24 AEAKAKAKAKAKAKAKAKAKA 248
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2) / M145;
 RX MEDLINE=21995410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Taronga A.-M., Challis G.L.,
 RA Thomson N.R., James D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larkie L., Ridgway J., Oliver K., O'Neill S.,
 RA Rabinowitz B., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squires R., Squires S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2).";
 RL Nature 417:141-147 (2002).
 DR EMBL; AL939118; CAB5369.1; -.
 GO; GO:004222; *F-metalloendopeptidase activity; IBA.*
 GO; GO:006508; *Proteolysis and peptidolysis; IBA.*
 DR InterPro; IPR002806; *Peptidase_M23.*
 DR InterPro; IPR011054; *Rudmnt_hyb_motif.*
 DR Pfam; PF01551; *Peptidase_M23; 1.*
 Complete proteome.

RESULT 25
 Q8PC3 PRELIMINARY; PRT; 1020 AA.
 ID Q8PC3
 AC Q8PC3;
 DT 01-JUN-2003 (TREMBrel. 24, Created)
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE RE13301P
 GN ORName=CG18375;
 OS *Drosophila melanogaster* (Fruit fly).
 OC *Eukarya; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oligopodida; Dipteroidea; Drosophilidae; Drosophila.*
 OC *Ephydriidae; Drosophilidae; Drosophila.*
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
 RA Champs M., Chavez C., Dorsett V., Drasne D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Gurin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munoz J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDJB databases.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 DR EMBL: BY003215; ASN024970.1; -.
 DR HSSP; P06241; ISHF.
 DR FlyBase; FBgn034606; CG18375.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR001452; SH3.
 DR PFam; PF00023; Ank; 2.
 DR Pfam; PF0018; SH3; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRODOM; PD00066; SH3; 1.
 DR SMART; SNO248; ANK; 2.
 DR SMART; SNO326; SH3; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 2.
 DR PROSITE; PS50297; ANK REP_REGION; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ANK repeat; SH3 domain.
 SQ SEQUENCE 1020 AA; 110433 MW; 42A3AB30EC71787B CRC64;
 Query Match 56.2%; Score 59; DB 2; Length 1020;
 Best Local Similarity 60.0%; Pred. No. 93;
 Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AXEAEAEKAAYAEEAEKAAXA 25
 Db 462 AAAAAAAQAQAEEAANQATAAA 486

RESULT 25

Q9W2J2 PRELIMINARY; PRT; 1020 AA.

AC Q9W2J2;

DT 01-MAY-2000 (TREMBLel. 13, Created)

DT 01-OCT-2002 (TREMBLel. 22, Last sequence update)

DT 01-MAR-2004 (TREMBLel. 26, Last annotation update)

DE CG18375; PA.

GN ORFnames=CG18375;

OS *Drosophila melanogaster* (Fruit fly).

OC Bukaryote; Metazoa; Arthropoda; Hexapoda; Insects; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Mecoptomorpha; Drosophilidae; Drosophilidae; Drosophila.

OC Ephydriidae; Drosophilidae; Drosophila.

OC NCBI_TaxId=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=0196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hosking R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter J., Helt G., Nelson C.R., Gabor G.L.,
 Abril J.F., Kobayashi A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beezon K.Y., Benos P.V., Bernick B., Bhandari D., Boleshkov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brostier P.,
 Burtsis K.C., Busam D.A., Butlier H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Douc L.E., Domes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferrara S., Fleischmann W.,
 Fosler C., Gabelli A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 Jalali M., Kalash F., Karpen G.H., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,
 Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merklikov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muñoz D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 Patel S., Adams M., Champe M., Dugan S.P., Fries E., Hodgson A.,
 George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 melanogaster euchromatic genome sequence.",
 Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).

RA RY [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=12537573; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirkas R.,
 Patel S., Fries E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 Ashburner M., Celniker S.E.,
 "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomics perspective.",
 Genome Biol. 3:RESEARCH0084 (2002).

RP RY [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 Smith C.D., Tupy J.L., Whited E.J., Bayraktaroglu L., Bernman B.P.,
 Brenton-Carroll G., Celniker S.E., de Grey A.D., Drysdale R.A.,
 Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Lewis S.E.,
 "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review.",
 Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).

RP RY [5]

RP SEQUENCE FROM N.A.

RX FlyBase; Submitted (ISBP-2002) to the EMBL/GenBank/DDJB databases.

RA FlyBase; Submitted (ISBP-2002) to the EMBL/GenBank/DDJB databases.

RA FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDJB databases.

CC -!- SIMILARITY: Contains 1 SH3 domain.

DR EMBL; AE003453; ASN024699.3; -.

DR HSSP; P06241; ISHF.

DR IntAct; Q9W2J2; -.

DR FlyBase; FBgn034606; CG18375.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR001452; SH3.

DR PFam; PF00023; Ank; 2.

DR PRINTS; PR01415; ANKYRIN.

DR PRODOM; PD00066; SH3; 1.

DR SMART; SNO0248; ANK; 2.

DR SMART; SNO0326; SH3; 1.

DR PROSITE; PS50088; ANK_REPEAT; 2.

DR PROSITE; PS50297; ANK REP_REGION; 1.

DR PROSITE; PS50002; SH3; 1.

KW ANK repeat; SH3 domain.

SQ SEQUENCE 1020 AA; 110374 MW; B18C928C514313DC CRC64;

Query Match 56.2%; Score 59; DB 2; Length 1020;
 Best Local Similarity 60.0%; Pred. No. 93;

AC Q85WT7; DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE RE6367P;
 Name=CG1738; ORFName=CG31361';
 OS Drosophila melanogaster (Fruit fly).
 OC Bokaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila;
 OC NCBI_TaxID=7227;
 RN [1] _SEQUENCE FROM N.A.
 RP PRELIMINARY;
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champs M., Chavez C., Dorsett V., Dreske D., Farfan D., Frise B.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuncio J., Pacelli J., Paragas V., Park S.,
 RA Patel S., Phanphanavong S., Wan K., Yu B., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY95087; AAM1415.1; -.
 DR HSSP; Q9QH9; 1EO.
 DR FlyBase; FBgn051351; CG31361.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003590; Ig_c2.
 DR Pfam; PF0047; Ig; 1.
 DR SMART; SM00408; IgG2; 1.
 DR PROSITE; FS50035; Ig_LIKE; 2.
 SQ SEQUENCE 694 AA; 75164 MW; 9C242F9F03051491 CRC64;
 Query Match 55.7%; Score 58.5; DB 2; Length 694;
 Best Local Similarity 66.7%; Pred. No. 78;
 Matches 16; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AXAAEAKAKYAAEAKAKAX 24
 DR 1:||||| :|||:|||:
 Db 343 AAADAAE-AAKLAABRAAOAAAK 365
 RESULT 33
 ID Q9P3E2
 AC Q9P3E2;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DB Related to transport protein USO1.
 GN Name=B13118.10;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OC NCBI_TaxID=5141;
 RN [1] _SEQUENCE FROM N.A.
 RP PRELIMINARY;
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nakatura G., Mewes H.W., Manhaupt G.; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL29089; CAB99171.1; -.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:00855; F:protein transporter activity; IEA.
 DR GO; GO:006886; F:intracellular protein transport; IEA.
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR006955; USO1_p115_C.
 DR InterPro; IPR006953; USO1_p115_head.
 DR Pfam; PF00871; USO1_p115_C; 1.
 DR Pfam; PF04869; USO1_p115_head; 1.
 SQ SEQUENCE 1171 AA; 131632 MW; 33DF50E5931BD060 CRC64;

Query Match 55.7%; Score 58.5; DB 2; Length 1171;
 Best Local Similarity 56.7%; Pred. No. 1.2e+02;
 Matches 17; Conservative 3; Mismatches 5; Indels 5; Gaps 1;
 QY 1 AXAAE---AEEKAKYAAEAKAKAXA 25
 DR 1:||||| :|||:|||:
 Db 1025 AEAEDAATGAEKAIAAEAAKAAS 1054

RESULT 34
 ID Q9D23
 AC Q9D23;
 DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Skin-type anti-freeze polypeptide AFP-2.
 OS Myoxocephalus scorpius (Shorthorn sculpin).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleosteii; Neoteleosteii;
 OC Acanthomorpha; Acanthopercyiformi; Percormorpha; Scorpaeniformes;
 OC Cottoidei; Cottidae; Myoxocephalus.
 DR NCBI_TaxID=8097;
 RN [1] _SEQUENCE FROM N.A.
 RP PRELIMINARY;
 RC TISSUE=Skin;
 RX MEDLINE=98389738; PubMed=9722537; DOI=10.1074/jbc.273.36.23098;
 RA Low W.-K., Miao M., Ewart K.V., Yang D.S.C., Fletcher G.L., Hew C.L.;
 RT "Skin-type antifreeze protein from the shorthorn sculpin, Myoxocephalus scorpius. Expression and characterization of a Mr 9, 700 recombinant protein.";
 RT J. Biol. Chem. 273:23098-23103 (1998).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Low W.-K., Miao M., Ewart K.V., Yang D.S.C., Fletcher G.L., Hew C.L.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF305502; ANG25982.1;
 DR GO; GO:0005625; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:005835; F:rice binding; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0042309; P:homoolthermy; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR GO; GO:0050826; P:response to freezing; IEA.
 DR InterPro; IPR000104; Antifreeze 1.
 DR InterPro; IPR001778; Rob_allergen_C.
 DR InterPro; IPR01839; Ribosomal_P2.
 DR PRINTS; PR00308; ANTIFREEZE1.
 DR PRINTS; PR00333; POLIUREGEN.
 DR PRINTS; PR00456; RIBOSOMAL_P2.
 SQ SEQUENCE 92 AA; 7693 MW; A3FCFD57B5CAB465 CRC64;

Query Match 55.2%; Score 58; DB 2; Length 92;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 AXAAEAKAKYAAEAKAKAXA 25
 DR 1:||||| :|||:
 Db 3 AAKAAEAAAMAANAAEAAKAA 27

RESULT 35
 ID Q7VKB8
 AC Q7VKB8;
 DT 01-OCT-2003 (TREMBrel. 25, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE Type I antifreeze protein.
 OS Ordericulusfames-PMT149; Prochlorococcus marinus (strain MIT 9313).

OC Bacteriia; Cyanobacteria; Prochlororales; Prochlorococcaceae;
 OC Prochlorococcus
 OC NCBI_TaxID=74547;
 RN [1] _SEQUENCE FROM N.A.
 RP MEDLINE:22823698; PubMed=12917642; DOI=10.1038/nature01947;
 RX Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinser E.R., Chisholm S.W.;
 RA "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
 RT niche differentiation."
 RL Nature 424:1042-1047 (2003).
 DR EMBL; BX572058; CAB21324.1; -.
 KW Complete proteome.
 SQ SEQUENCE 124 AA; 12053 MW; 0023FB3DBP04B16E CRC64;
 Query Match 55.2%; Score 58; DB 2; Length 387;
 Best Local Similarity 56.5%; Pred. No. 22; Mismatches 4; Indels 0; Gaps 0;
 Matches 13; Conservative 19; Sensitive 4; Gaps 2;
 Qy 1 AXAAEAK---AKYAAE-AAEKAAGXA 25
 Db 55 AAABAAKQAKQAQAAKAAEAAKKAEEAA 87
 RESULT 36
 PRELIMINARY; PRT; 387 AA.
 ID 096113
 AC 096113;
 DT 01-MAY-1999 (TREMBREL. 10, Created)
 DT 01-MAR-2003 (TREMBREL. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)
 DE Riffin.
 GN Name=PFB0035c;
 OS Plasmodium falciparum (isolate 3D7);
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=36329;
 RN [1] _SEQUENCE FROM N.A.
 RP MEDLINE:9902143; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
 RX Gardner M.J., Tettelin H., Carrucci D.J., Cummings L.M., Aravind L.,
 RA Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Pederson J.,
 RA Shen K., Jing J., Aston C., Iai T., Schwartz D.C., Petrea M.,
 RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
 RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.,
 RA "Chromosome 2 sequence of the human malaria parasite Plasmodium
 RT falciparum.";
 RL Science 282:1126-1132 (1998).
 RN [2] _SEQUENCE FROM N.A.
 RP MEDLINE:22255705; PubMed=12368864; DOI=10.1038/nature01097;
 RX Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
 RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaideya A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.; Hoffmann S.L., Newbold C., Davis R.W.,
 RT "Genome sequence of the human malaria parasite Plasmodium
 RT falciparum.";
 RL Nature 419:498-511 (2002).
 DR PIR: A71625; A71625;
 DR InterPro: IPR011038; Calycin.
 DR InterPro: IPR006313; Riffin.
 DR InterPro: IPR002850; Riffin_STEVOR.
 DR Pfam: PF02009; Riffin_STEVOR; 1.
 DR TIGRFAMS; TIGR01477; Riffin; 1.
 SQ SEQUENCE 387 AA; 42873 MW; 98846A6B588C2A35 CRC64;

Query Match 55.2%; Score 58; DB 2; Length 387;
 Best Local Similarity 56.5%; Pred. No. 56; Mismatches 6; Indels 0; Gaps 0;
 Matches 13; Conservative 19; Sensitive 4; Gaps 2;
 Qy 2 XAAEAKAKYAAEKAAGXA 24
 Db 304 IVEGAEQAKAAKAAEKGVTAA 326
 RESULT 37
 PRELIMINARY; PRT; 558 AA.
 ID QPRWB7
 AC QPRWB7;
 DT 01-MAR-2004 (TREMBREL. 26, Created)
 DT 01-MAR-2004 (TREMBREL. 26, Last sequence update)
 DT 25-OCT-2004 (TREMBREL. 28, Last annotation update)
 DE Hypothetical protein (probable proline-tRNA ligase).
 GN Name=NCU04449.1; Synonyms=621B4.130;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariidae; Sordariaceae; Neurospora.
 OC NCBI_TaxID=5141;
 RN [1] _SEQUENCE FROM N.A.
 RP STRAIN=OR74A;
 RC Galagan J.E., Calvo S.B., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA .Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburn M.,
 RA Seiftrunkopf C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kotche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gneire S.,
 RA Kamal M., Kanwellsis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
 RA Krystofova S., Rasmussen C., Metzger R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
 RA Desouza C.C., Glass L., Orthach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Narvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RL Nature 0:0-0 (2004).
 RN [2] _SEQUENCE FROM N.A.
 RP SCHULTE U., AIGN V., HOHEISL J., BRANDT P., FARTMANN B., HOLLAND R.,
 RA NYAKATURA G., MEVES H.W., MANNHAUPT G.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3] _SEQUENCE FROM N.A.
 RP Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RA German Neurospora genome project;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to class-II aminocetyl-tRNA synthetase family.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX0100792; EAA26671.1; -.
 DR EMBL; BAF08808; GAF05998.1; -.
 DR HSSP; Q33N97; 1H4S.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0004827; F:proline-tRNA ligase activity; IEA.
 DR GO; GO:0006412; F:protein biosynthesis; IEA.
 DR InterPro; IPR04154; HGT; anticoagulation.
 DR InterPro; IPR04149; PRO_fam I.
 DR InterPro; IPR02134; tRNA-synt_2b.
 DR InterPro; IPR02116; tRNA-synt_pro.
 DR InterPro; IPR006195; tRNA_ligase_II.
 DR Pfam; PF03129; HGT; anticoagulation; 1.
 DR Pfam; PF00587; tRNA-synt_2b; 1.
 DR Pfam; PRO046; TRNA-synt_II.
 DR TIGRFAMS; TIGR00408; pros_fam_I; 1.

DE DT 01-MAR-2004 (REMBLREL. 26, last annotation update)

RSC12 (Fragment)

RC Dicystostelium discoideum (Slime mold).

RC Dicystostelium discoideum (Slime mold).

RC Eukaryota; Mycetozoa; Dictyostelliida; Dictyostelium.

RC NCB1_TAXID=44689;

RC [1]

RN RP SEQUENCE FROM N.A.

RC STRAIN-NA;

RC Iranfar N.; Loomis W.F.;

RC Submitted (DEC-1995) to the EMBL/GenBank/DDJB databases.

RL DR

RL EMBL; U83087; BAB4930.1; -

DR DictryBase; DDB0214855; Irc12.

DR GO; GO:0005737; C:cytoplasm; IEA.

DR GO; GO:0006817; P:phosphate transport; IER.

DR InterPro; IPR008160; Collagen; 1.

DR Pfam; PF01391; Collagen; 1.

FT NON_TER

FT SEQUENCE 809 AA; 80296 MW; 5488FF7BA344300 CRC64;

Query Match 55.2%; Score 58; DB 2; Length 809;

Best Local Similarity 56.0%; Pred. No. 1e+02; Region of the tomato ringspot nepovirus RNA-1-encoded polyprotein in

Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0; Vitro.;"

YQ 1 AXAAEAEKAAYAAEAEKAAXAXA 25

Db 765 STAAGQAGAAAGAAQKAMAA 789

RT R1

RT "Proteolytic processing at a novel cleavage site in the N-terminal

RT region of the tomato ringspot nepovirus RNA-1-encoded polyprotein in

RT vitro.;"

RT J. Gen. Virol. 81:2771-2781(2000).

RL R2

RL [6]

RL SUBCELLULAR LOCATION OF THE NBT-VPG PROTEIN.

RL R3

RL PubMed=1103391;

RL R4

RL Han S., Sanfacon H.; Wang A., Sanfacon H.;

RL "Tomato ringspot virus proteins containing the nucleoside triphosphate

RL binding domain are transmembrane proteins that associate with the

RL endoplasmic reticulum and cofractionate with replication complexes.;"

RL R5

RL J. Virol. 77:523-534 (2003).

RN R6

RN [17]

RN TOPOLOGY OF THE NBT-VPG PROTEIN, GLYCOSYLATION, AND MUTAGENESIS OF

RN RP

RN THR-1230.

RX R7

RX PubMed=1769910; DOI=10.1093/vir.0.19612-0;

RA R8

RA Wang A., Han S., Sanfacon H.;

RA R9

RA "Topogenesis of the NBT-VPG protein of Tomato ringspot

RA nepovirus: definition of the C-terminal transmembrane domain.;"

RL R10

RL J. Gen. Virol. 85:55-545 (2004).

CC R11

CC --!- FUNCTION: The NBT-VPG polyprotein may act as a membrane-anchor for

CC R12

CC --!- CATALYTIC ACTIVITY: N nucleoside triphosphate +

CC R13

CC [RNA] (N).

CC R14

CC --!- SUBCELLULAR LOCATION: The NBT-VPG polyprotein is associated with

CC endoplasmic-derived membranes that are active in viral

CC replication. VPG localizes to the endoplasmic reticulum lumen. NBT

CC R15

CC is an integral membrane protein.

CC R16

CC --!- PM: Specific enzymatic cleavages by 3C-like protease in vivo

CC yield mature proteins. 3C-like protease is autocatalytically

CC processed. NBT exists as NBT-Vpg polyprotein as well as NBT mature

CC R17

CC --!- PTM: Vpg is covalently linked to the 5' end of genomic RNA (By

CC R18

CC similarity).

CC R19

CC --!- SIMILARITY: Belongs to the nepoviruses RNA1 polyprotein family.

CC R20

CC --!- CAUTION: It is uncertain whether Mat-1 or Met-122 is the

CC initiator.

CC R21

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC R22

CC EMBL; L19655; AAA78254.1; -.

DR R23

DR M73822; AAA47941.1; -.

DR R24

DR M73822; AAA47942.1; ALT_INIT.

DR R25

DR PIR; A40797; GIVVSR.

DR R26

DR MEROPS; C03_012; -.

DR R27

DR InterPro; IPR004004; Pept_Calici.

DR R28

DR EMBL; L19655; AAA78254.1; -.

DR R29

DR InterPro; IPR010464; Picornain_3C.

DR R30

DR InterPro; IPR000605; RNA_helicase.

DR R31

DR InterPro; IPR007095; RNA_poi_DS_PS.

DR R32

DR InterPro; IPR001205; RNA_poi_P3D.

DR R33

DR InterPro; IPR007094; RNA_poi_P5vir.

DR R34

DR Pfam; PF00343; Picornain_3C; 1.

DR R35

DR Pfam; PF00680; RNA_dep_RNA_poi; 1.

DR R36

DR Pfam; PF00910; RNA_nuclease; 1.

DR R37

DR PRINTS; PRO01918; CALIVIRUS.

KW R38

KW ATP-binding; Covalent protein-RNA linkage; Direct protein sequencing;

KW Glycoprotein; Hydrolase; Polypeptide; Proteinase; Protease; Transferase;

KW RNA-directed RNA polymerase; Thiol protease; Transfase;

RT R39

RT Published=10092022;

RA R40

RA Wang A., Carrier K., Chisholm J., Wieczorek A., Huguenot C.,

RA Sanfacon H.;

RA "Proteolytic processing of tomato ringspot nepovirus 3C-like protease

precursors; definition of the domains for the Vpg, protease and

putative RNA-dependent RNA polymerase.;"

KW		Query Match	
Transmembrane.		54.8%; Score 57.5; DB 2; Length 638;	
FT CHAIN 1 423 X1 protein.		X2 protein.	
FT CHAIN 424 620 X2 protein.		NTP-binding protein.	
FT CHAIN 621 1212 Viral genome-linked protein.		3C-like protease.	
FT CHAIN 1213 1239 RNA-directed RNA polymerase.		Cyttoplasmic.	
FT CHAIN 1240 1486 Probable.		Luminal.	
FT DOMAIN 1487 2197 FT TRANSMEM 1167 1188 FT DOMAIN 1189 1212 FT DOMAIN 149 152 FT DOMAIN 230 235 FT ACT-SITE 1283 1283 FT ACT-SITE 1331 1331 FT ACT-SITE 1433 1433 SITE 1451 SITE 1451		NP_BIND 796 803 ID 15860 PRELIMINARY; PRT; 190 AA.	
FT DOMAIN 230 235 FT ACT-SITE 1331 1331 FT ACT-SITE 1433 1433 SITE 1451 SITE 1451		NP_BIND 796 803 ID 15860 PRELIMINARY; PRT; 190 AA.	
FT CARBOHYD 1228 1228 FT MUTAGEN 423 423 FT MUTAGEN 620 620 FT MUTAGEN 1212 1212 FT MUTAGEN 1230 1230 FT MUTAGEN 1283 1283 FT MUTAGEN 1451 1451 FT MUTAGEN 1465 1465 FT MUTAGEN 1486 1486 FT CONFLICT 1230 1230 SQ SEQUENCE 2197 AA; 241428 MW; 2D8P92855DBCB9 CRC64;		NP_BIND 796 803 ID 15860 PRELIMINARY; PRT; 190 AA.	
Query Match 55.2%; Score 58; DB 1; Length 2197; Best Local Similarity 50.0%; Pred. No. 2.3e+02; Matches 14; Conservative 1; MisMatches 5; Indels 0; Gaps 0; Sq		Missing: No cleavage between X1 and X2. Missing: No cleavage between X2 and NTB. Missing: No cleavage NTB and VPG.	
Qy 6 AEKAKYAAEAEKAKAYA 25 Db 180 ARKAKYAAFAARKKAAVA 199		T-A: Complete loss of N-linked glycosylation. H-D: Complete loss of protease activity. H-L: Complete loss of protease activity. Q->A: No effect. O-A: No cleavage between 3C-like protease and RNA-directed RNA polymerase. T -> A (in Ref. 4; AA sequence).	
RESULT 42 ID 089IE3 PRELIMINARY; PRT; 638 AA.		RESULT 43 ID 015860 PRELIMINARY; PRT; 190 AA.	
AC 089IE3; DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)		AC 015860; PRELIMINARY; PRT; 190 AA.	
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		AC 015860; PRELIMINARY; PRT; 190 AA.	
DE B11595 protein.		AC 015860; PRELIMINARY; PRT; 190 AA.	
GN OrderredicuNames=bl1696;		AC 015860; PRELIMINARY; PRT; 190 AA.	
OS Bradyrhizobium japonicum.		AC 015860; PRELIMINARY; PRT; 190 AA.	
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.		AC 015860; PRELIMINARY; PRT; 190 AA.	
OX NCBI_TaxID=375;		AC 015860; PRELIMINARY; PRT; 190 AA.	
RN 1) SSEQUENCE FROM N.A.		AC 015860; PRELIMINARY; PRT; 190 AA.	
RP STRAIN=USDA10;		AC 015860; PRELIMINARY; PRT; 190 AA.	
RX MEDLINE=224B4998; PubMed=12597275;		AC 015860; PRELIMINARY; PRT; 190 AA.	
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Kawashima K., Kohara M., Matsubara M., Shimojo S., Ibusuoka H., Wada T., Yamada M., Tabata S., "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.", DNA Res. 9:189-197(2002); EMBL: AB005055; BAC50961.1; GO: GO:003063; Protease activity; IFA. GO: GO:0006508; Protein modification by proteolysis and peptidolysis; IFA. InterPro: IPR001309; TCE_P20; PROSITE: PS50208; CASPASE_P20; Complete proteome.		AC 015860; PRELIMINARY; PRT; 190 AA.	
SQ 638 AA; 68387 MW; 9519C8A749528B5B CRC64;		AC 015860; PRELIMINARY; PRT; 190 AA.	
RESULT 44 ID 08X965 PRELIMINARY; PRT; 394 AA.		RESULT 44 ID 08X965 PRELIMINARY; PRT; 394 AA.	
AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
GN Name=t01K; OrderredicuNames=EC6074, 2907; Escherichia coli O157:H7.		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
OC [1] NCBI_TaxID=83334;		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
RN SEQUENCE FROM N.A.		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
RP STRAIN=0157:H7; EDL933 / ATCC 700927 / EHEC;		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
RX MEDLINE=2107935; PubMed=11206551; DOI=10.1038/35054089; Perna N.G., Flunkert G., III, Burnell V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.",		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
RA [1] Nature 409:529-533(2001).		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
RN [2]		AC 08X965; DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	

RC STRAIN=015:H7 / RIMD 0509952 / EHEC;
 RX MEDLINE=2115231; PubMed=11258795;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Otsubuo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Otsuji H., Honda T., Sabakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001);
 DR EMBL; A5005232; AAQ55075.1; -.
 DR EMBL; A5002533; BAB34197.1; -.
 DR PIR; F90725; F90725.
 DR PIR; G85576; G85576.
 DR HS3P; P19934; 1TOL.
 DR InterPro; IPR010528; T0LA.
 DR Pfam; PF06519; T0LA; 1.
 KW Complete proteome.
 SQ SEQUENCE 394 AA; 40517 MW; 5958D8E89230BDE28 CRC64;
 Query Match 54.3%; Score 57; DB 2; Length 394;
 Best Local Similarity 56.0%; Pred. No. 74;
 Matches 14; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 AAKAAEAKAKYAAEAKAKAKA 25
 Db 151 ADDKAAEAAKKAADAKKKEEAA 175

RESULT 45

Q875A8 PRELIMINARY; PRT; 508 AA.
 ID Q875A8;
 AC 0875A8;
 DT 01-JUN-2003 (TREMBL; 24, Created)
 DT 01-JUN-2003 (TREMBL; 24, Last sequence update)
 DE Similar to Dani_rerio protein-kinase.
 OS Podospora anserina.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
 OX NCBI_TaxID=5145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Genoscope;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BX088700; CAD60707.1; -.
 DR HS3P; P08622; 1BQZ.
 GO; GO:0016301; F-kinase activity; IEA.
 DR InterPro; IPR001633; DnaJ_N.
 DR InterPro; IPR008940; Prenyl_trans.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF0025; DnaJ_1.
 DR Pfam; PF00515; TPR_1; 1.
 DR SMART; SM00271; DnaJ_1.
 DR SMART; SM00028; TPR; 3.
 DR PROSITE; PS50016; DNAJ_2; 1.
 DR PROSITE; PS50005; TPR; 2.
 DR PROSITE; SS50293; TPR_REGION; 1.
 KW Kinase; Repeat; TPR repeat.
 SQ SEQUENCE 508 AA; 55747 MW; 5826AC06E1EBDB9 CRC64;
 Query Match 54.3%; Score 57; DB 2; Length 508;
 Best Local Similarity 70.0%; Pred. No. 91;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 AAEKAKYAAEAKAKAK 24
 Db 136 AAEKAKYAAEAKAKAG 155

Search completed: July 11, 2005, 09:46:25
 Job time : 170 secs

AP

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OM protein - protein search, using BW model
 Run on: July 11, 2005, 09:22:59 ; Search time 161 Seconds
 (without alignments)
 60.056 Million cell updates/sec

Title: SBQ1
 perfect score: 105
 Sequence: 1 axaaeaaekaaayaaeakakaxa 25
 Scoring table: BLOSUM62DX
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : A_Geneseq_16Dec04: *
 1: geneseqD1980s: *
 2: geneseqD1990s: *
 3: geneseqD2000s: *
 4: geneseqD2001s: *
 5: geneseqD2002s: *
 6: geneseqD2003as: *
 7: geneseqD2003bs: *
 8: geneseqD2004as: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
 ID AAB66787 standard; peptide; 25 AA.
 XX
 AC AAB66787;
 XX
 DT 11-APR-2001 (first entry)
 XX
 DE Amphipathic peptide conjugate.
 XX
 KW Amphipathic; lipid bilayer; detergent.
 XX
 OS Synthetic.
 XX
 PN WO200102425-A2.
 XX
 PD 11-JAN-2001.
 XX
 PR 29-JUN-1999; 99US-014988P.
 XX
 PA (UWHE-) UNIV HEALTH NETWORK.
 XX
 PI Priv G;
 XX
 DR WPI; 2001-138120/14.
 XX
 PT New amphipathic peptide conjugate having detergent properties, and hydrophobic and hydrophilic phase, useful e.g. for stabilizing and crystallizing proteins and membrane proteins, as cytolytic agents, surfactants or emulsifiers.
 XX
 PS Claim 1; Page 22; 29pp; English.
 XX
 The present invention relates to an amphipathic peptide conjugate having detergent properties and a hydrophobic and hydrophilic face. The amphipathic peptide conjugate can be used for the stabilization and crystallization of proteins and membrane proteins, for modifying the properties of lipid bilayer membranes, as cytolytic agents, as molecules that can facilitate the transport of polar molecules across biological membranes, and as emulsifiers and surfactants

Sequence 25 AA;

Query Match 100.0%; Score 105; DB 4; Length 25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

26 63 60.0 67 7 ADE10647
 27 63 60.0 67 8 ADE10666 Nucleatin
 28 63 60.0 67 8 ADE10676
 29 63 60.0 75 7 ADE10696
 30 63 60.0 75 7 ADE10646
 31 63 60.0 75 8 ADE10645
 32 63 60.0 75 8 ADE10665 Nucleatin
 33 63 60.0 83 7 ADE10695
 34 63 60.0 83 7 ADE10645
 35 63 60.0 83 8 ADE10674
 36 63 60.0 83 8 ADE10664 Nucleatin
 37 63 60.0 88 7 ADE10642
 38 63 60.0 88 7 ADE10692
 39 63 60.0 88 8 ADE10671
 40 63 60.0 88 8 ADE10661 Nucleatin
 41 63 60.0 91 7 ADE10694
 42 63 60.0 91 7 ADE10644
 43 63 60.0 91 8 ADE10644 Nucleatin
 44 63 60.0 91 8 ADE10663 Nucleatin
 45 63 60.0 104 7 ADE10690 Nucleatin
 ADE10647 Structure
 ADE10666 Nucleatin
 ADE10676 Library f
 ADE10696 Structure
 ADE10646 Structure
 ADE10645 Library f
 ADE10664 Nucleatin
 ADE10642 Structure
 ADE10692 Structure
 ADE10671 Library f
 ADE10661 Nucleatin
 ADE10694 Structure
 ADE10644 Structure
 ADE10663 Nucleatin
 ADE10693 Library f
 ADE10690 Structure

QY 1 AXAAEAKAKYAAEAKAKAYA 25
 CC ||||| ||||| ||||| |||||
 CC 1 AXAAEAKAKYAAEAKAKAYA 25

RESULT 2
 ADR10685
 ID ADEL0685 standard; protein; 104 AA.
 XX
 AC ADE10685;
 XX DT 29-JAN-2004 (first entry)
 XX DE Structurally biased random peptide library scaffold protein seqid 92.
 XX KW fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response;
 KW scaffold protein.
 XX OS Synthetic.
 XX PN US2003143562-A1.
 XX PD 31-JUL-2003.
 XX PF 20-JUN-2002; 2002US-00177725.
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 (RIGE-) RIGEL PHARM INC.
 XX PA Anderson D, Peele BR, Bogenberger JM;
 XX PT DR WPI; 2003-829786/77.
 XX Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX PS Disclosure; SEQ ID NO 92; 110pp; English.
 XX The invention describes a library (I) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;
 CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptide which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene

RESULT 3
 ADE10635
 ID ADR10635 standard; protein; 104 AA.
 XX ADR10635;
 XX AC ADE10635;
 XX DT 29-JAN-2004 (first entry)
 DE Structurally biased random peptide library related protein seqid 42.
 XX KW fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotype; cell morphology; cell growth; cell viability; cell death;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response.
 XX OS Synthetic.
 XX PN US2003143562-A1.
 XX PD 31-JUL-2003.
 XX PF 20-JUN-2002; 2002US-00177725.
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 (RIGE-) RIGEL PHARM INC.
 XX PA Anderson D, Peele BR, Bogenberger JM;
 XX PT DR WPI; 2003-829786/77.
 XX Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX PS Example 6; SEQ ID NO 42; 110pp; English.
 XX The invention describes a library (II) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;

CC where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e. half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacological activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes (APC) and the Drosophila discs-large gene (Dlg), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin biology applications, neurobiology applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.

XX sequence 104 AA;

CC Query Match 63.8%; Score 67; DB 7; Length 104;
CC Best Local Similarity 68.0%; Pred. No. 0.18;
CC Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
CC QY 1 AXAFRAEKAKYAAEAKAKAKAXA 25
CC DB 10 AAAAAGAAEAKAKAAEAKAAEAA 34

RESULT 4

XX ADK15654
XX ID ADK15654 standard; peptide; 104 AA.
XX AC ADK15654;
XX DT 06-MAY-2004 (first entry)
XX DB Nucleating sequence-containing library fusion protein #36.
XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
XX KW green fluorescent protein; GFP; alpha helical biasing sequence;
XX KW nucleating sequence; screening.
XX OS Synthetic.
XX PN US2003224412-A1.
XX PD 04-DEC-2003.
XX PF 18-MAR-2003; 2003US-00393449.
XX PR 08-OCT-1998; 98US-00169015.
XX PR 08-OCT-1999; 99US-00415765.
XX PR 20-JUN-2002; 2002US-00177725.
XX PA (ANDE/) ANDERSON D.
XX PA (PEEL/) PEELE B R.
XX PA (BOEG/) BOGENBERGER J M.
XX PI Anderson D, Peelle BR, Bogenberger JM;
XX DR WPI; 2004-033956/03.

XX WPI; 2004-033956/03.

XX PR Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.

XX Disclosure; SEQ ID NO 92; 110pp; English.

XX CC The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating sequence.

XX SQ Sequence 104 AA;

XX Query Match 63.8%; Score 67; DB 8; Length 104;
XX Best Local Similarity 68.0%; Pred. No. 0.18;
XX Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX QY 1 AXAFRAEKAKYAAEAKAKAXA 25
XX DB 10 AAAAAGAAEAKAKAAEAA 34

RESULT 5

XX ADK15704
XX ID ADK15704 standard; peptide; 104 AA.
XX AC ADK15704;
XX DT 06-MAY-2004 (first entry)
XX DB Library fusion protein-related scaffold protein #36.
XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
XX KW green fluorescent protein; GFP; alpha helical biasing sequence;
XX KW nucleating sequence; screening.
XX OS Synthetic.
XX PN US2003224412-A1.
XX PD 04-DEC-2003.
XX PF 18-MAR-2003; 2003US-00393449.
XX PR 08-OCT-1998; 98US-00169015.
XX PR 08-OCT-1999; 99US-00415765.
XX PR 20-JUN-2002; 2002US-00177725.
XX PA (ANDE/) ANDERSON D.
XX PA (PEEL/) PEELE B R.
XX PA (BOEG/) BOGENBERGER J M.
XX PI Anderson D, Peelle BR, Bogenberger JM;
XX DR WPI; 2004-033956/03.

XX PR Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.

XX Disclosure; SEQ ID NO 92; 110pp; English.

XX CC The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent

CC protein - GRP) and a library peptide sequence comprising an alpha helical
CC biasing sequence, or a Scaffold protein, a library peptide and a
CC nucleating sequence. The library of protein of the invention is useful for screening
CC biactive peptides conferring a particular phenotype. The present amino
CC acid sequence represents a scaffold protein.

Qy	1 AXABAAEKAKYAAEAKAKAXA 25	6; Indels	0; Gaps
Db	10 AAAAAEAAKAKAAEAKAAEA 34		

RESULT 6

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

ID ABU27824 standard; protein; 428 AA.
XX
AC ABU27824;
XX
DT 19-JUN-2003 (first entry)
XX

	Best Local Similarity	Pred. No.	Mismatches	Matches	Indels	Gaps
Oy	1 AXAAEAKAA----KYYAAEAKKAKAX	24	2;	18;	Conservative	4;
Db	210 AEAEEKKAQAEKKAEEAKKQAAAE	238				

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Enterobacter cloacae.
 XX
 XX
 XX
 XX
 XX

RESULT 7
ADO43180
ID ADO43180 standard; peptide; 28 AA.
XX
AC ADO43180;
XX
DT 29-JUL-2004 (first entry)

PF 21-MAR-2002; 2002WO-US009107.
XX
21 MAR 2001. 2001TC 00015742

DE Peptide used for coded probe synthesis.
 XX Nano-barcode; scanning probe microscopy
 KW OS Synthetic.

PA (ELIT-) ELITRA PHARM INC
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX

F1 Wang Li, Zainulabid, Malone C, Habedanck K, Onisen KU, Zyskina JW;
PT Wang B, Dawbrick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI: 2003-02996/02.
DR N-PSD: AC311694

PT new diverse nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
PT
PS XX

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the nucleic acid

PT alignment. Matrix-bar-codes encoding specific information for Scanning
 PS probe microscopy, useful in the fields of molecular biology.

Example 2; Page 44; 63pp; English.

XX

CC The present sequence is that of a peptide of potential use for production
 CC of a coded probe useful in the method of the invention. The invention
 CC provides methods, apparatus and compositions for the detection.

CC antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of

provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). The methods allow the sequencing of long nucleic acid sequences in a single sequencing run, high speed of obtaining sequence data, low cost of sequencing and high efficiency in terms of operator time, and sensitive

CC and accurate detection and/or identification of nucleic acids with low incidence of false positive results.

CC

CC incidence of false positive results.

XX

XX

SQ Sequence 28 AA;

Query Match 61.0%; Score 64; DB 8; Length 28;
Best Local Similarity 65.2%; Pred. No. 0.1;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 XAAEAAKAKYAAEAAKAKAX 23

RESULT 8

ADD43177 ADD43177 standard; peptide; 28 AA.

AC ADD43177;

XX 29-JUL-2004 (first entry)

DT

DE Peptide used for coded probe synthesis.

XX

DE Nano-barcode; scanning probe microscopy; probe.

XX

OS Synthetic.

XX

PN WO2004038037-A2.

XX

PD 06-MAY-2004.

XX

PR 22-SEP-2003; 2003WO-US029726.

XX

PR 20-SEP-2002; 2002US-00251152.

XX

PR 19-SEP-2003; 2003US-00667004.

XX

PA (ITLC) INTEL CORP.

XX

PI Chan S, Su X, Yamakawa M;

XX

DR WPI; 2004-399960/37.

XX

PT Detecting, identifying and sequencing of biomolecules using controlled PT alignment of nano-barcodes encoding specific information for scanning PT probe microscopy, useful in the fields of molecular biology.

XX

PS Example 2; Page 44; 63pp; English.

XX

The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The invention provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). The methods allow the sequencing of long nucleic acid sequences in a single sequencing run, high speed of obtaining sequence data, low cost of sequencing and high efficiency in terms of operator time, and sensitive and accurate detection and/or identification of nucleic acids with low incidence of false positive results.

XX

SQ Sequence 28 AA;

Query Match 61.0%; Score 64; DB 8; Length 28;
Best Local Similarity 65.2%; Pred. No. 0.1;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 XAAEAAKAKYAAEAAKAKAX 24

RESULT 9

ADD1063 ADD1063 standard; protein; 104 AA.

AC ADD1063;

XX 29-JAN-2004 (first entry)

DT

DE Structurally biased random peptide library scaffold protein seqid 90.

XX

DE fusion nucleic acid library; scaffold protein; bioactive peptide; KW phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; KW loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; KW Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; KW skin biology; cosmetics; endocrinology; infectious disease; KW drug toxicity; drug resistance; inflammation; allergic response; KW scaffold protein.

XX

OS Synthetic.

XX

PN US2003143562-A1.

XX

PD 31-JUL-2003.

XX

PR 20-JUN-2002; 2002US-00177725.

XX

PR 08-OCT-1998; 98US-00169015.

XX

PR 08-OCT-1999; 99US-00415765.

XX

PA (RIGE) RIGEL PHARM INC.

XX

PI Anderson D, Peele BR, Bogenberger JM;

XX

DR WPI; 2003-829786/77.

XX

PT Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening PT methods.

XX

PS Disclosure; SEQ ID NO 90; 110pp; English.

XX

The invention describes a library (1) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence, and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence, where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epictic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coli gene (APC) and the Drosophila discs-large gene (DIG), which are components of cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, infectious disease applications, drug toxicities and drug

CC	resistance applications, immunobiology, inflammation, and allergic
CC	library can easily be monitored both for its presence within cells and
CC	its quantity. The expression of structurally biased libraries generate
CC	elevated cellular concentration of peptides having a given structural
CC	bias and thus increase the hit rate for targets that bind such
CC	structures. This is the amino acid sequence of a scaffold protein used in
CC	peptide libraries to hold the library peptide in a conformationally
CC	restricted form.
SQ	Sequence 104 AA;
Query	March
Best	Local Similarity
Matches	72.0%; Pred. No. 0.45%; Mismatches 3; Indels 2; Gaps
OY	1 AXAAEAKAKAKAAEAKAKAKA 25
Db	9 AAAEAKAKA-AAAEEAKAKAA 31
RESULT 10	
ADE10682	
ID	ADE10682 standard; protein: 104 AA.
XX	
AC	ADE10682;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Structurally biased random peptide library scaffold protein seqid 89.
XX	
KW	fusion nucleic acid library; scaffold protein; biactive peptide;
KW	phenotype change; cell morphology; cell growth; cell viability;
KW	cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KW	loss of cell division; decreased cell growth; brca-1; brca-2;
KW	tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KW	Drosophila disc-1large; big; cardiovascular; neurobiology; bone biology;
KW	skin biology; cosmeceutical; endocrinology; infectious disease;
KW	drug toxicity; drug resistance; inflammation; allergic response;
KW	scaffold protein.
XX	
OS	Synthetic.
XX	
PN	US2003143562-A1.
XX	
PD	31-JUL-2003.
XX	
PP	20-JUN-2002; 2002US-00177725.
XX	
PR	08-OCT-1998; 98US-0016015.
PR	08-OCT-1999; 99US-00415765.
XX	
PA	(RIGS-) RIGEL PHARM INC.
XX	
PI	Anderson D, Peele BR, Bogenberger JM;
XX	
DR	WPI; 2003-829786/77.
XX	
PT	Novel library of fusion nucleic acids each of which has fused first and
PT	second nucleic acids encoding scaffold protein and library peptide having
PT	alpha helical biasing sequence, respectively, useful in screening
PT	methods.
XX	
PS	Disclosure: SEQ ID NO 89; 110PP; English.
XX	
CC	The invention describes a library (1) of fusion nucleic acids, where each
CC	scaffold protein sequence, and a second nucleic acid (N1), encoding a
CC	scaffold nucleic acid comprises a first nucleic acid (N1), encoding a
CC	library peptide sequence comprising an alpha helical biasing sequence;
CC	where N1 is fused to N2. Disclosed is a method for screening biactive
CC	peptides conferring a change in specific phenotype such as cell
CC	morphology, cell growth, cell viability, adhesion to substrates or other
CC	cells, and cellular density; changes in the expression of one or more

PI Anderson D, Peelle BR, Bogenberger JM;
 XX DR WPI; 2003-829786/77.

XX PT alpha helical biasing sequence, respectively, useful in screening

PT methods.

XX

PS Example 6; SEQ ID NO 40; 110pp; English.

XX

CC

</

Db 9 |:||| ||| ||| |||:|
 RESULT 13 9 AAAAEEAKKA--AAAEEAKKA 31
 ID ADK15652
 XX ADK15652 standard; peptide; 104 AA.
 AC ADK15652;
 XX
 DT 06-MAY-2004 (first entry)
 DB Nucleating sequence-containing library fusion protein #34.
 XX fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.
 XX
 OS Synthetic.
 XX
 US2003224412-A1.
 PN
 XX
 PD 04-DEC-2003.
 XX
 PF 18-MAR-2003; 2003US-00393449.
 XX
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 PR 20-JUN-2002; 2002US-00177725.
 XX
 PA (ANDE/) ANDERSON D.
 PA (PEEL/) PEELE B. R.
 PA (BOGE/) BOGENBERGER J M.
 XX
 PD 04-DEC-2003.
 XX
 PP 18-MAR-2003; 2003US-00393449.
 XX
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 PR 20-JUN-2002; 2002US-00177725.
 XX
 PA (ANDE/) ANDERSON D.
 PA (PEEL/) PEELE B. R.
 PA (BOGE/) BOGENBERGER J M.
 XX
 PI Anderson D, PEELE B R, Bogenberger JM;
 DR WPI; 2004-033956/03.
 XX
 PT Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.
 XX
 PT Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.
 XX
 PS Example 6; SEQ ID NO 40; 110pp; English.
 XX
 CC The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a
 CC nucleating sequence. The library of the invention is useful for screening
 CC bioactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a scaffold protein.
 XX
 SQ Sequence 104 AA;
 Query Match 61.0%; Score 64; DB 8; Length 104;
 Best Local Similarity 72.0%; Pred. No. 0.45; 2; Mismatches 3; Indels 2; Gaps 1;
 Matches 18; Conservative 2;
 QY 1 AXAAEAEKAAYKAEEAKKA 25
 Db 9 AAAAEEAKKA--AAAEEAKKA 31
 RESULT 15
 ADK15702
 XX
 AC ADK15702
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Library fusion protein-related scaffold protein #34.
 XX
 DB 1 AXAAEAEKAAYKAEEAKKA 25
 DB 9 AAAAEEAKKA--AAAEEAKKA 31
 RESULT 14
 ADK15701
 ID ADK15701 standard; peptide; 104 AA.
 XX
 AC ADK15701;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DB Library fusion protein-related scaffold protein #33.
 XX
 Library fusion protein-related scaffold protein #33.

XX fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.
 XX
 OS Synthetic.
 XX
 US2003224412-A1.
 PN
 XX
 PD 04-DEC-2003.
 XX
 PR 18-MAR-2003; 2003US-00393449.
 XX
 PR 08-OCT-1998; 98US-00169015.

CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer, such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (DIG), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmeceutical applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a scaffold protein used in
 CC peptide libraries to hold the library peptide in a conformationally
 CC restricted form.

CC Sequence 104 AA;

Query Match 60.5%; Score 63.5; DB 7; Length 104;
 Best Local Similarity 72.0%; Pred. No. 0.52; 18; Mismatches 4; Indels 1; Gaps 1;

QY 1 AXAAEAEKAKYAAEAEKAKAKA 25
 1 :|:|||:|||:|||:|||:|||:
 6 AAAAAEAAAK-AAAABAAKAA 29
 Db

RESULT 18
 DE ADE10634 standard; peptide; 104 AA.
 ID ADE10634
 AC ADE10634;
 XX DT 29-JAN-2004 (first entry)

DE Structurally biased random peptide library related protein seqid 41.
 KW fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2; APC;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response.
 OS Synthetic.
 XX US2003143562-A1.
 XX 31-JUL-2003.

XX 20-JUN-2002; 2002US-0017725.
 XX PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.

CC (RIGE-) RIGEL PHARM INC.
 PA XX
 PI XX
 DR XX
 WPI: 2003-829786/77.
 PR Novel library of fusion nucleic acids each of which has fused first and
 PR second nucleic acids encoding scaffold protein and library peptide having
 PR alpha helical biasing sequence, respectively, useful in screening
 PR methods.

PS Example 6; SEQ ID NO 41; 110PP; English.

XX The invention describes a library (1) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;
 CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer, such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (DIG), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmeceutical applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a protein associated with
 CC fused nucleic acid and random peptide libraries of the invention.

XX Sequence 104 AA;

Query Match 60.5%; Score 63.5; DB 7; Length 104;
 Best Local Similarity 72.0%; Pred. No. 0.52; 18; Mismatches 4; Indels 1; Gaps 1;

QY 1 AXAAEAEKAKYAAEAEKAKAKA 25
 1 :|:|||:|||:|||:|||:|||:
 6 AAAAAEAAAK-AAAABAAKAA 29
 Db

RESULT 19
 ADK15703
 ID ADK15703 standard; peptide; 104 AA.
 XX
 AC ADK15703;
 XX
 DT 06-MAY-2004 (first entry)
 DE Library fusion protein-related scaffold protein #35.
 XX
 KW fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;

KW nucleating sequence; screening.
XX
OS Synthetic.
XX
PN US2003224412-A1.
XX
PD 04-DEC-2003.
XX
PP 18-MAR-2003; 2003US-00393449.
XX
PR 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
PR 20-JUN-2002; 2002US-00177725.
XX
PR (ANDE/)
PA (PEEL/)
PA (PEEL/)
PA (BOGE/)
XX
PI Anderson D, Peelle BR, Bogenberger JM;
DR WPI; 2004-033956/03.
XX
PT Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
PS Example 6; SEQ ID NO 41; 110pp; English.
XX
CC The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening biactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating sequence.
CC
PT Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
PS Disclosure; SEQ ID NO 91; 110pp; English.
XX
CC The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening biactive peptides conferring a particular phenotype. The present amino acid sequence represents a scaffold protein.
XX
SQ Sequence 104 AA;
XX
Query Match 60.5%; **Score** 63.5; **DB** 8; **Length** 104;
Best Local Similarity 72.0%; **Pred.** No. 0.52;
Matches 18; **Conservative** 2; **Mismatches** 4; **Indels** 1; **Gaps** 1;
Db 6 AAAAEEAAK-AAAEEAAKAAA 29
RESULT 21
ID ADE10698
XX
AC ADE10698;
XX
DT 29-JAN-2004 (first entry)
XX
DE Structurally biased random peptide library scaffold protein seqid 105.
XX
KW fusion nucleic acid library; scaffold protein; biactive peptide;
KW phenotype change; cell morphology; cell growth; cell viability;
KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
KW loss of cell division; decreased cell growth; brca-1; brca-2;
KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
KW drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology;
KW skin biology; cosmeceutical; endocrinology; infectious disease;
KW drug toxicity; drug resistance; inflammation; allergic response;
KW scaffold protein.
XX
OS Synthetic.
XX
PN US2003143562-A1.
XX
PD 31-JUL-2003.
XX
PR 20-JUN-2002; 2002US-00177725.
XX
PR 08-OCT-1998; 98US-00169015.
PR 08-OCT-1999; 99US-00415765.
XX
PI (RIGE-) RIGEL PHARM INC.
XX
PI Anderson D, Peelle BR, Bogenberger JM;
DR WPI; 2003-829786/77.
XX
PT Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having

PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX
 PS Disclosure; SEQ ID NO 105; 110pp; English.
 XX
 CC The invention describes a library (I) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;
 CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dtg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmeceutical applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a scaffold protein used in
 CC peptide libraries or hold the library peptide in a conformationally
 CC restricted form.
 XX
 SQ Sequence 59 AA;

Query Match 60.0%; Score 63; DB 7; Length 59;
 Best Local Similarity 66.7%; Pred. No. 0.32;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEAEKAAYAEEAEKAAXA 25
 : ||| ||| ||| ||| ||| : |
 Db 4 DAAMEAAKAAKAAEAKAAMAA 27

RESULT 22
 ADE10648
 ID ADE10648 standard; protein; 59 AA.
 XX
 AC ADE10648;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Structurally biased random peptide library related protein seqid 55.
 XX
 KW fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; Dtg; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; inflammation; allergic response;
 KW drug toxicity; drug resistance; drug; inflammation; allergic response.
 XX

OS Synthetic.
 XX
 PN US2003143562-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 20-JUN-2002; 2002US-0017725.
 XX
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 XX
 PA (RIGE-) RIGEL PHARM INC.
 XX
 PI Anderson D, Peele BR, Bogenberger JM;
 XX
 DR WPI; 2003-829786/77.
 XX
 PT Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX
 PS Example 6; SEQ ID NO 55; 110pp; English.
 XX
 CC The invention describes a library (I) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;
 CC where N1 is fused to N2. Disclosed is a method for screening bioactive
 CC peptides conferring a change in specific phenotype such as cell
 CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dtg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmeceutical applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a protein associated with
 CC fused nucleic acid and random peptide libraries of the invention.
 XX
 SQ Sequence 59 AA;

Query Match 60.0%; Score 63; DB 7; Length 59;
 Best Local Similarity 66.7%; Pred. No. 0.32;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 XAEAEKAAYAEEAEKAAXA 25
 : ||| ||| ||| ||| ||| : |
 Db 4 DAAMEAAKAAKAAEAKAAMAA 27

RESULT 23

ADK15717
 ID ADK15717 standard; peptide; 59 AA.
 XX
 AC
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DB Library fusion protein-related scaffold protein #49.
 XX
 KW fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.
 XX
 OS Synthetic.
 XX
 PN US2003224412-A1.
 XX
 PR 04-DEC-2003.
 XX
 PR 18-MAR-2003; 2003US-00393449.
 XX
 PR 08-OCT-1998; 98US-00169015.
 XX
 PR 08-OCT-1999; 99US-00415765.
 PR 20-JUN-2002; 2002US-00177725.
 XX
 PA (ANDR/) ANDERSON D.
 PA (PEEL/) PEELIE B. R.
 PA (BOGE/) BOGENBERGER J M.
 XX
 PI Anderson D, Peelle BR, Bogenberger JM;
 XX
 DR WPI; 2004-033956/03.
 XX
 XX
 PT Library of fusion polypeptides in which each polypeptides comprises
 scaffold protein and library peptide having alpha helical biasing
 sequence, or scaffold protein, library peptide and nucleating sequence.
 XX
 PA (ANDR/) ANDERSON D.
 PA (PEEL/) PEELIE B. R.
 PA (BOGE/) BOGENBERGER J M.
 XX
 PI Anderson D, Peelle BR, Bogenberger JM;
 XX
 DR WPI; 2004-033956/03.
 XX
 PT Library of fusion polypeptides in which each polypeptides comprises
 scaffold protein and library peptide having alpha helical biasing
 sequence, or scaffold protein, library peptide and nucleating sequence.
 XX
 PS Disclosure; SEQ ID NO 105; 110pp; English.
 XX
 CC The invention comprises a library of fusion nucleic acids, where each
 encoded protein contains a scaffold protein (e.g. a green fluorescent
 protein - GFP) and a library peptide sequence comprising an alpha helical
 biasing sequence, or a scaffold protein, a library peptide and a
 nucleating sequence. The library of the invention is useful for screening
 biocactive peptides conferring a particular phenotype. The present amino
 acid sequence represents a library protein containing a nucleating
 CC sequence.
 XX
 SQ Sequence 59 AA;
 XX
 Query Match 60.0%; Score 63; DB 8; Length 59;
 Best Local Similarity 66.7%; Pred. No. 0.32;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 2 XAEEAEKAKYAAEAEKAKA 25
 DB 4 DAALAEAAKAAEAAKAAEAA 27
 RESULT 25
 ADE10697
 ID ADE10697 standard; protein; 57 AA.
 XX
 AC ADE10697;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Structurally biased random peptide library scaffold protein seqid 104.
 XX
 KW fusion nucleic acid library; scaffold protein; biactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomas; polyps; coli; APC;
 KW Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response;
 KW scaffold protein.
 XX
 OS Synthetic.
 XX
 US2003143562-A1.
 XX
 PN 31-JUL-2003.
 XX
 PR 20-JUN-2002; 2002US-00177725.
 XX
 OS Synthetic.

PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 XX PA (RIGE-) RIGEL PHARM INC.
 XX PI Anderson D, Peele BR, Bogenberger JM;
 XX DR WPI; 2003-829786/77.
 PT Novel library of fusion nucleic acids each of which has fused first and
 second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX Disclosure; SEQ ID NO 104; 110pp; English.
 XX
 CC The invention describes a library (1) of fusion nucleic acids, where each
 fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 scaffold protein sequence; and a second nucleic acid (N2), encoding a
 library peptide sequence comprising an alpha helical biasing sequence;
 where N1 is fused to N2. Disclosed is a method for screening bioactive
 peptides conferring a change in specific phenotype such as cell
 morphology, cell growth, cell viability, adhesion to substrates or other
 cells, and cellular density; changes in the expression of one or more
 RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 lipids, hormones, cytokines, or other molecules; etc. The bioactive
 peptide identified by above mentioned method is used to generate more
 candidate peptides and to identify target molecules i.e., the molecules
 with which the bioactive peptide interacts. The peptide(s) can be
 combined with other pharmacological activators to study the epistatic
 relationships of signal transduction pathways in question. The disclosed
 method is also useful in cancer applications. Random libraries can be
 introduced into any tumour cell (primary or cultured), and peptides
 identified which by themselves induce apoptosis, cell death, loss of cell
 division or decreased cell growth. The method is also useful for
 screening of bioactive peptides which restore the constitutive function
 of the brca-1 or brca-2 genes, and other tumour suppressor genes
 important in breast cancer such as the adenomatous polyposis coli gene
 (APC) and the Drosophila discs-large gene (Dlg), which are components of
 cell-cell junctions. The methods are useful in cardiovascular
 applications, neurobiology applications, bone biology applications, skin
 biology applications, cosmeceutical applications, endocrinology
 applications, infectious disease applications, drug toxicities and drug
 resistance applications, immunobiology, inflammation, and allergic
 response applications, and biotechnology applications. The peptide
 library can easily be monitored, both for its presence within cells and
 its quantity. The expression of structurally biased libraries generate
 elevated cellular concentration of peptides having a given structural
 structures. This is the amino acid sequence of a scaffold protein used in
 peptide libraries or hold the library peptide in a conformationally
 restricted form.
 XX Sequence 67 AA;

SQ Query Match 60.0%; Score 63; DB 7; Length 67;
 Best Local Similarity 66.7%; Pred. No. 0.37; Mismatches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 XAEAAKAKYAAEAAKAKAXA 25
 : ||| ||| ||| ||| ||| : |||
 Db 4 DAANAEAAKAKAEEAKAKAEEA 27
 RESULT 26
 ADB10647 ADB10647 standard; protein; 67 AA.
 XX AC ADB10647;
 XX DT 29-JAN-2004 (first entry)
 XX
 DE Structurally biased random peptide library related protein seqid 54.
 XX fusion nucleic acid library; scaffold protein; bioactive peptide;
 XX phenotype change; cell morphology; cell growth; cell viability;
 XX cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 XX loss of cell division; decreased cell growth; brca-1; brca-2;
 XX tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 XX Drosophila discs-large; Dlg; cardiovascular; neurobiology; bone biology;
 XX skin biology; cosmeceutical; endocrinology; infectious disease;
 XX drug toxicity; drug resistance; inflammation; allergic response.
 OS Synthetic.
 XX PN US2003143562-A1.
 XX PD 31-JUL-2003.
 XX PR 20-JUN-2002; 2002US-00177725.
 XX PR 08-OCT-1998; 98US-00169015.
 XX PR 08-OCT-1999; 99US-00415765.
 XX PA (RIGE-) RIGEL PHARM INC.
 XX PI Anderson D, Peele BR, Bogenberger JM;
 XX DR WPI; 2003-829786/77.
 XX
 CC The invention describes a library (1) of fusion nucleic acids each of which has fused first and
 second nucleic acids encoding scaffold protein and library peptide having
 alpha helical biasing sequence, respectively, useful in screening
 methods.
 XX Example 6; SEQ ID NO 54; 110pp; English.
 XX
 CC The invention describes a library (1) of fusion nucleic acids, where each
 fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 scaffold protein sequence; and a second nucleic acid (N2), encoding a
 library peptide sequence comprising an alpha helical biasing sequence;
 where N1 is fused to N2. Disclosed is a method for screening bioactive
 peptides conferring a change in specific phenotype such as cell
 morphology, cell growth, cell viability, adhesion to substrates or other
 cells, and cellular density; changes in the expression of one or more
 RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 lipids, hormones, cytokines, or other molecules; etc. The bioactive
 peptide identified by above mentioned method is used to generate more
 candidate peptides and to identify target molecules, i.e., the molecules
 with which the bioactive peptide interacts. The peptide(s) can be
 combined with other pharmacological activators to study the epistatic
 relationships of signal transduction pathways in question. The disclosed
 method is also useful in cancer applications. Random libraries can be
 introduced into any tumour cell (primary or cultured), and peptides
 identified which by themselves induce apoptosis, cell death, loss of cell
 division or decreased cell growth. The method is also useful for
 screening of bioactive peptides which restore the constitutive function
 of the brca-1 or brca-2 genes, and other tumour suppressor genes
 important in breast cancer such as the adenomatous polyposis coli gene
 (APC) and the Drosophila discs-large gene (Dlg), which are components of
 cell-cell junctions. The methods are useful in cardiovascular
 applications, neurobiology applications, bone biology applications, skin
 biology applications, cosmeceutical applications, endocrinology
 applications, infectious disease applications, drug toxicities and drug
 resistance applications, immunobiology, inflammation, and allergic
 response applications, and biotechnology applications. The peptide
 library can easily be monitored, both for its presence within cells and
 its quantity. The expression of structurally biased libraries generate
 elevated cellular concentration of peptides having a given structural
 structures. This is the amino acid sequence of a protein associated with
 fused nucleic acid and random peptide libraries of the invention.
 XX Sequence 67 AA;

Query Match 60.0%; Score 63; DB 7; Length 67;
 Best Local Similarity 66.7%; Pred. No. 0.37;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XAEAEKAAYAEEAEKAAXA 25
 Db :||| ||||| ||||| :||| :||| 27

RESULT 27
 ADK1566 ID ADK1566 standard; peptide; 67 AA.
 XX AC
 XX ADK1566;
 XX DT 06-MAY-2004 (first entry)
 XX DE
 DE Nucleating sequence-containing library fusion protein #48.
 XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.
 XX OS Synthetic.
 XX PN US2003224412-A1.
 XX PD 04-DEC-2003.
 XX PF 18-MAR-2003; 2003US-00193449.
 XX PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-0015765.
 PR 20-JUN-2002; 2002US-0017725.
 XX PA (ANDE/) ANDERSON D.
 PA (PEBL/) PEEBLE B. R.
 PA (BOGE/) BOGENBERGER J M.
 XX PI Anderson D, Peeble BR, Bogenberger JM;
 XX DR WPI; 2004-033956/03.
 XX PT Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.
 XX PS Disclosure; SEQ ID NO 104; 110PP; English.
 XX CC The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a
 CC nucleating sequence. The library of the invention is useful for screening
 CC bioactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a scaffold protein.
 XX SQ Sequence 67 AA;
 Query Match 60.0%; Score 63; DB 8; Length 67;
 Best Local Similarity 66.7%; Pred. No. 0.37;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XAEAEKAAYAEEAEKAAXA 25
 Db :||| ||||| ||||| :||| :||| 27

RESULT 28
 ADK15716 ID ADK15716 standard; peptide; 67 AA.

Query Match 60.0%; Score 63; DB 7; Length 67;
 Best Local Similarity 66.7%; Pred. No. 0.37;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XAEAEKAAYAEEAEKAAXA 25
 Db :||| ||||| ||||| :||| :||| 27

RESULT 29
 ADK15716 ID ADK15716 standard; protein; 75 AA.
 XX AC
 XX ADE10696;
 XX DT 29-JAN-2004 (first entry)
 XX DE Structurally biased random peptide library scaffold protein seqid 103.
 XX KW fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;

DE structurally biased random peptide library scaffold protein seqid 102.
 XX fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brc-a-1; brc-a-2;
 KW tumor suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response;
 KW scaffold protein.
 XX OS Synthetic.
 XX PN US2003143562-A1.
 XX PD 31-JUL-2003.
 XX PP 20-JUN-2002; 2002US-00177725.
 XX PR 08-OCT-1998; 98US-00169015.
 XX PR 08-OCT-1999; 99US-00415765.
 XX PA (RIGE) RIGEL PHARM INC.
 XX PI Anderson D, Peele BR, Bogenberger JM;
 XX DR WPI; 2003-829786/77.
 PT Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX Disclosure; SEQ ID NO 102; 110PP; English.
 PS
 The invention describes a library (I) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;
 CC where N1 is fused to N2. Disclosed is a method for screening biactive
 CC peptides conferring a change in specific phenotype such a cell
 morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured) and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brc-a-1 or brc-a-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmeceutical applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 structures. This is the amino acid sequence of a scaffold protein used in

CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the bcr-a-1 or bcr-a-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dlg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a protein associated with
 CC fused nucleic acid and random peptide libraries of the invention.

SQ Sequence 83 AA:

Query Match 60.0%; Score 63; DB 7; Length 83;
 Best Local Similarity 66.7%; Pred. No. 0.47;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AXAAEAEKAAYAAEAEKAKAK 24
 Db 57 AAKAAEAEKAAYAAEAEKAKAK 80

RESULT 35

ID ADK15714 standard; peptide; 83 AA.

XX ADK15714;
 AC 06-MAY-2004 (first entry)

DE Library fusion protein-related scaffold protein #46.

XX fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.

XX Synthetic.

OS US200322412-A1.

XX PD 04-DEC-2003.

XX PR 18-MAR-2003; 2003US-00393449.

XX PR 08-OCT-1998; 98US-00169015.

XX PR 08-OCT-1998; 98US-0015765.

XX PR 20-JUN-2002; 2002US-0017725.

XX (ANDE/) ANDERSON D.
 PA (PEEL/) PEELLE B. R.
 PA (BOGE/) BOGENBERGER J. M.

XX PT Anderson D, Peelle BR, Bogenberger JM;

XX DR WPI; 2004-033956/03.

XX PT Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.

XX PS Example 6; SEQ ID NO 52; 110pp; English.

CC encoded protein contains a scaffold protein (e.g. a green, fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a
 CC nucleating sequence. The library of the invention is useful for screening
 CC bioactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a scaffold protein.

CC Sequence 83 AA;

Query Match 60.0%; Score 63; DB 8; Length 83;
 Best Local Similarity 66.7%; Pred. No. 0.47;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AXAAEAEKAAYAAEAEKAKAK 24
 Db 57 AAKAAEAEKAAYAAEAEKAKAK 80

RESULT 36

XX ADK15664 standard; peptide; 83 AA.

AC ADK15664;

XX DT 06-MAY-2004 (first entry)

DE Nucleating sequence-containing library fusion protein #45.

XX fusion nucleic acid library; fusion protein library; scaffold protein;
 KW green fluorescent protein; GFP; alpha helical biasing sequence;
 KW nucleating sequence; screening.

XX Synthetic.

OS US200322412-A1.

XX PD 04-DEC-2003.

XX PR 18-MAR-2003; 2003US-00393449.

XX PR 08-OCT-1998; 98US-00169015.

XX PR 08-OCT-1998; 98US-0015765.

XX PR 20-JUN-2002; 2002US-0017725.

XX (ANDE/) ANDERSON D.
 PA (PEEL/) PEELLE B. R.
 PA (BOGE/) BOGENBERGER J. M.

XX PT Anderson D, Peelle BR, Bogenberger JM;

XX DR WPI; 2004-033956/03.

XX PT Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.

XX PS Example 6; SEQ ID NO 52; 110pp; English.

CC The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green, fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a
 CC nucleating sequence. The library of the invention is useful for screening
 CC bioactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a library protein containing a nucleating
 CC sequence.

CC Sequence 83 AA;

Query Match 60.0%; Score 63; DB 8; Length 83;
 Best Local Similarity 66.7%; Pred. No. 0.47;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

XX Disclosure; SEQ ID NO 102; 110pp; English.

CC The invention comprises a library of fusion nucleic acids, where each

CC morphology, cell growth, cell viability, adhesion to substrates or other
 CC cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The bioactive,
 CC peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the bioactive peptide interactors. The peptide(s) can be
 CC combined with other pharmacologic interactors to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (dlg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmeceutical applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology, applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a scaffold protein used in
 CC peptide libraries or hold the library peptide in a conformationally
 CC restricted form.

XX SQ sequence 88 AA;

XX Best Local Similarity 60.0%; Score 63; DB 7; Length 88;
 XX Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 XX Qy 1 AXAAEAEEKAAYKAEEAEEKAAX 24
 XX : ||| ||| ||| ||| ||| : 86
 XX Db 63 AAKAAAEAAAKAAEAAAKAAAK 86

XX RESULT 39
 XX ID ADK15711
 XX ID ADK15711 standard; peptide: 88 AA.
 XX AC ADK15711;
 XX DT 06-MAY-2004 (first entry)
 XX DE Nucleating sequence-containing library fusion protein #43.
 XX KW fusion nucleic acid library; fusion protein library; scaffold protein;
 XX KW green fluorescent protein; GFP; alpha helical biasing sequence;
 XX KW nucleating sequence; screening.
 XX OS Synthetic.
 XX PN US2003224412-A1.
 XX PD 04-DEC-2003.
 XX PF 18-MAR-2003; 2003US-00393449.
 XX PR 08-OCT-1998; 98US-00169015.
 XX PR 08-OCT-1999; 99US-00415765.
 XX PR 20-JUN-2002; 2002US-0017725.
 XX PA (ANDE/) ANDERSON D.
 XX PA (PEEL/) PEELE B R.
 XX PA (BOGE/) BOGENBERGER J M.
 XX PI Anderson D, PEELE B R, BOGENBERGER JM;
 XX DR 04-DEC-2003.
 XX PR 18-MAR-2003; 2003US-00393449.
 XX PR 08-OCT-1998; 98US-00169015.
 XX PR 08-OCT-1999; 99US-00415765.
 XX PR 20-JUN-2002; 2002US-0017725.

XX (ANDE/) ANDERSON D.
 XX (PEEL/) PEELE B R.
 XX (BOGE/) BOGENBERGER J M.

XX PS Example 6; SEQ ID NO 49; 110bp; English.

XX CC The invention comprises a library of fusion nucleic acids, where each
 XX CC encoded protein contains a scaffold protein (e.g. a green fluorescent
 XX CC protein - GFP) and a library peptide sequence comprising an alpha helical
 XX CC biasing sequence, or a scaffold protein, a library peptide and a

Query Match 60.0%; Score 63; DB 8; Length 88;
 Best Local Similarity 66.7%; Pred. No. 0.5;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 AXAEEAKAKYAAEAAKAKAX 24
 Db 63 AAKAAEAAAKAAEAAKAAAK 86

RESULT 41
 ADE10694
 ID ADE10694 standard; protein; 91 AA.
 XX
 AC ADE10694;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DB Structurally biased random peptide library scaffold protein seqid 101.
 XX
 KW fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response;
 KW scaffold protein.
 XX
 OS Synthetic.
 XX
 PN US2003143562-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 20-JUN-2002; 2002US-00177725.
 XX
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 PA (RIGE-) RIGEL PHARM INC.

XX
 PI Anderson D, Peelle BR, Bogenberger JM;
 XX
 DR WPI; 2003-829786/77.

XX
 Novel library of fusion nucleic acids each of which has fused first and
 second nucleic acids encoding scaffold protein and library peptide having
 alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX
 PS Disclosure; SEQ ID NO 101; 110pp; English.

XX
 The invention describes a library (1) of fusion nucleic acids, where each
 fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 scaffold protein sequence; and a second nucleic acid (N2), encoding a
 library peptide sequence comprising an alpha helical biasing sequence;
 where N1 is fused to N2. Disclosed is a method for screening bioactive
 peptides conferring a change in specific phenotype such as cell
 morphology, cell growth, cell viability, adhesion to substrates or other
 cells, and cellular density; changes in the expression of one or more
 RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 lipids, hormones, cytokines, or other molecules; etc. The bioactive
 peptide identified by above mentioned method is used to generate more
 candidate peptides and to identify target molecules, i.e., the molecules

CC nucleating sequence. The library of the invention is useful for screening
 CC bioactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a library protein containing a nucleating
 CC sequence.
 XX Sequence 88 AA:
 CC Query Match 60.0%; Score 63; DB 8; Length 88;
 CC Best Local Similarity 66.7%; Pred. No. 0.5;
 CC Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 CC Qy 1 AXAEEAKAKYAAEAAKAKAX 24
 CC Db 63 AAKAAEAAAKAAEAAKAAAK 86

RESULT 42
 ADE10644
 ID ADE10644 standard; protein; 91 AA.
 XX
 AC ADE10644;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Structurally biased random peptide library related protein seqid 51.
 XX
 KW fusion nucleic acid library; scaffold protein; bioactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response.
 XX
 OS Synthetic.
 XX
 PN US2003143562-A1.
 XX
 PD 31-JUL-2003.
 XX
 PR 20-JUN-2002; 2002US-00177725.
 XX
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 XX
 PA (RIGE-) RIGEL PHARM INC.
 XX
 PI Anderson D, Peelle BR, Bogenberger JM;
 XX
 DR WPI; 2003-829786/77.

XX
 Novel library of fusion nucleic acids each of which has fused first and
 second nucleic acids encoding scaffold protein and library peptide having
 alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX
 PS Disclosure; SEQ ID NO 101; 110pp; English.

XX
 The invention describes a library (1) of fusion nucleic acids, where each
 fusion nucleic acid comprises a first nucleic acid (N1), encoding a
 scaffold protein sequence; and a second nucleic acid (N2), encoding a
 library peptide sequence comprising an alpha helical biasing sequence;
 where N1 is fused to N2. Disclosed is a method for screening bioactive
 peptides conferring a change in specific phenotype such as cell
 morphology, cell growth, cell viability, adhesion to substrates or other
 cells, and cellular density; changes in the expression of one or more
 RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 lipids, hormones, cytokines, or other molecules; etc. The bioactive
 peptide identified by above mentioned method is used to generate more
 candidate peptides and to identify target molecules, i.e., the molecules

CC with which the bioactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacological activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of bioactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 (APC) and the Drosophila discs-large gene (Dtg), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmetic applications, endocrinology
 CC applications, infectious disease applications, drug toxicities and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a scaffold protein used in
 CC peptide libraries or hold the library peptide in a conformationally
 CC restricted form.

XX Sequence 91 AA:
 CC Query Match 60.0%; Score 63; DB 7; Length 91;
 CC Best Local Similarity 66.7%; Pred. No. 0.52;
 CC Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 CC Qy 1 AXAEEAKAKYAAEAAKAKAX 24
 CC Db 65 AAKAAEAAAKAAEAAKAAAK 88

DR WPI: 2004-033956/03.
 XX
 PT Library of fusion polypeptides in which each polypeptides comprises
 PT scaffold protein and library peptide having alpha helical biasing
 PT sequence, or scaffold protein, library peptide and nucleating sequence.
 XX
 PS Disclosure; SEQ ID NO 101; 110pp; English.
 XX
 CC The invention comprises a library of fusion nucleic acids, where each
 CC encoded protein contains a scaffold protein (e.g. a green fluorescent
 CC protein - GFP) and a library peptide sequence comprising an alpha helical
 CC biasing sequence, or a scaffold protein, a library peptide and a
 CC nucleating sequence. The library of the invention is useful for screening
 CC biactive peptides conferring a particular phenotype. The present amino
 CC acid sequence represents a scaffold protein.
 XX
 SQ Sequence 91 AA;

Query Match	60.0%	Score	63;	DB	8;	Length	91;
Best Local Similarity	66.7%	Pred.	0.52;	Matches	16;	Conservative	2;
Mismatches	6;	Indels	0;	Gaps	0;		

QY 1 AXAAEAKAKYAAEAKAKAX 24
 65 AAKAAEAKAAKAAEAKAAK 88

RESULT 45
 ADE10690 ADE10690 standard; protein; 104 AA.
 ID ADE10690;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 DE Structurally biased random peptide library scaffold protein seqid 97.
 XX
 KW fusion nucleic acid library; scaffold protein; biactive peptide;
 KW phenotype change; cell morphology; cell growth; cell viability;
 KW cell adhesion; cellular density; cancer; tumour; apoptosis; cell death;
 KW loss of cell division; decreased cell growth; brca-1; brca-2;
 KW tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
 KW Drosophila discs-large; Dig; cardiovascular; neurobiology; bone biology;
 KW skin biology; cosmeceutical; endocrinology; infectious disease;
 KW drug toxicity; drug resistance; inflammation; allergic response;
 KW scaffold protein.
 XX
 OS Synthetic.
 XX
 PN US2003143562-A1.
 XX
 PD 31-JUL-2003.
 XX
 PP 20-JUN-2002; 2002US-00177725.
 XX
 PR 08-OCT-1998; 98US-00169015.
 PR 08-OCT-1999; 99US-00415765.
 XX
 PA (RIGB-) RIGEL PHARM INC.
 XX
 PI Anderson D, Peele BR, Bogenberger JM;
 XX
 DR WPI; 2003-829786/77.
 XX
 PT Novel library of fusion nucleic acids each of which has fused first and
 PT second nucleic acids encoding scaffold protein and library peptide having
 PT alpha helical biasing sequence, respectively, useful in screening
 PT methods.
 XX
 PS Disclosure; SEQ ID NO 97; 110pp; English.
 XX
 CC The invention describes a library (I) of fusion nucleic acids, where each
 CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a

CC scaffold protein sequence; and a second nucleic acid (N2), encoding a
 CC library peptide sequence comprising an alpha helical biasing sequence;
 CC where N1 is fused to N2. Disclosed is a method for screening biactive
 peptides conferring a change in specific phenotype such as cell
 morphology, cell growth, viability, adhesion to substrates or other
 cells, and cellular density; changes in the expression of one or more
 CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
 CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein,
 CC lipids, hormones, cytokines, or other molecules; etc. The biactive
 peptide identified by above mentioned method is used to generate more
 CC candidate peptides and to identify target molecules, i.e., the molecules
 CC with which the biactive peptide interacts. The peptide(s) can be
 CC combined with other pharmacologic activators to study the epistatic
 CC relationships of signal transduction pathways in question. The disclosed
 CC method is also useful in cancer applications. Random libraries can be
 CC introduced into any tumour cell (primary or cultured), and peptides
 CC identified which by themselves induce apoptosis, cell death, loss of cell
 CC division or decreased cell growth. The method is also useful for
 CC screening of biactive peptides which restore the constitutive function
 CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
 CC important in breast cancer such as the adenomatous polyposis coli gene
 CC (APC) and the Drosophila discs-large gene (Dig), which are components of
 CC cell-cell junctions. The methods are useful in cardiovascular
 CC applications, neurobiology applications, bone biology applications, skin
 CC biology applications, cosmeceutical applications, endocrinology and drug
 CC resistance applications, immunobiology, inflammation, and allergic
 CC response applications, and biotechnology applications. The peptide
 CC library can easily be monitored, both for its presence within cells and
 CC its quantity. The expression of structurally biased libraries generate
 CC elevated cellular concentration of peptides having a given structural
 CC bias and thus increase the hit rate for targets that bind such
 CC structures. This is the amino acid sequence of a scaffold protein used in
 CC peptide libraries or hold the library peptide in a conformationally
 XX
 SQ Sequence 104 AA;

Query Match	60.0%	Score	63;	DB	7;	Length	104;
Best Local Similarity	66.7%	Pred.	0.61;	Matches	16;	Conservative	2;
Mismatches	6;	Indels	0;	Gaps	0;		

QY 1 AXAAEAKAKYAAEAKAKAX 24
 79 AAKAAEAKAAKAAEAKAAK 102

Search completed: July 11, 2005, 09:43:30
 Job time : 163 secs

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OM protein - protein search, using SW model

Run on: July 11, 2005, 09:37:04 ; Search time 42 Seconds
(without alignments)
44.434 Million cell updates/sec

Title: SEQ1
Perfect score: 105
Sequence: 1 axaeaakaakyaaeaaekaakaxa 25

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1i/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

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6: /cgn2_6/ptodata/1/1aa/backTsel.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	64.8	69	4	US-09-902-540-14824
2	61.5	58.5	56	4	US-09-902-540-743A3
3	61.5	58.6	56	4	US-09-816-989A-3
4	61.5	58.6	86	4	US-09-405-743A-6
5	61.5	58.6	86	4	US-09-816-989A-6
6	61	58.1	33	1	US-08-303-025-16
7	61	58.1	33	2	US-08-436-703B-4
8	61	58.1	469	4	US-09-489-039A-13565
9	60.5	57.6	117	4	US-09-340-736E-9
10	60.5	57.6	117	4	US-09-964-662-9
11	60.5	57.6	118	4	US-09-340-736E-10
12	57.6	118	4	US-09-964-662-10	
13	60.5	57.6	199	4	US-09-340-736E-11
14	60.5	57.6	199	4	US-09-964-662-11
15	60.5	57.6	200	4	US-09-340-736E-2
16	60.5	57.6	200	4	US-09-964-662-2
17	60.5	57.6	201	2	US-08-911-364-2
18	60.5	57.6	730	4	US-09-961-403-8
19	60.5	57.6	731	2	US-08-911-364-1
20	60.5	57.6	731	4	US-09-340-736E-1
21	60.5	57.6	731	4	US-09-964-662-1
22	60.5	57.6	733	3	US-08-464-70-2
23	59.5	56.7	67	4	US-09-869-875-7
24	59	56.2	45	4	US-09-405-743A-2
25	59	56.2	45	4	US-09-816-989A-2
26	59	56.2	109	4	US-09-405-743A-7
27	56.2	109	4	US-09-816-989A-7	

ALIGNMENTS

RESULT 1
US-09-902-540-14824
Sequence 14824, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; SEQ ID NO: 14824
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO: 14824
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Myxococcus xanthus

RESULT 2
US-09-902-540-14824
Query Match 64.8%; Score 68; DB 4; Length 69;
Best Local Similarity 64.0%; Pred. No. 0.018; Gaps 0;
Matches 16; Conservative 4; Mismatches 5; Indels 0;
OY 1 AXAEAAKAAYAAEAAKAAKAYA 25
Db 12 AAKGAAEAAKRAAEAAKRAAEAA 36

GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATRIMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60507-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 3
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
OTHER INFORMATION: Peptide

US-09-405-743A-3

Query Match Best Local Similarity 58.6%; Score 61.5; DB 4; Length 56;

Matches 16; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 2 XAAEAAEKA--AKYAAEAAEAKAKAYA 25
Db 29 AAEAKKKAAEAKYKAAKAKAAKEAA 53

RESULT 3

US-09-816-989A-3

; Sequence 3, Application US/09816989A

; Patent No. 6800287

; GENERAL INFORMATION:

; APPLICANT: Gad, Alexander

; APPLICANT: Lis, Doris

; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

; TITLE OF INVENTION: AND FOR THERAPEUTIC USE

; FILE REFERENCE: 2609/60807-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/816, 989A

; PRIOR APPLICATION NUMBER: 60/101, 693

; PRIOR FILING DATE: 1998-09-25

; PRIOR APPLICATION NUMBER: PCT/US99/22402

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SEQ ID NO 6

; LENGTH: 56

; PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide

; US-09-816-989A-3

Query Match Best Local Similarity 58.6%; Score 61.5; DB 4; Length 56;

Matches 16; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 2 XAAEAAEKA--AKYAAEAAEAKAKAYA 25
Db 29 AAEAKKKAAEAKYKAAKAKAAKEAA 53

RESULT 4

US-09-405-743A-6

; Sequence 6, Application US/09405743A

; Patent No. 6516938

; GENERAL INFORMATION:

; APPLICANT: Yeda Research and Development Co., Ltd.

; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS

; FILE REFERENCE: 60307-A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SEQ ID NO 6

; LENGTH: 86

; PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

; US-09-405-743A-6

Query Match Best Local Similarity 58.6%; Score 61.5; DB 4; Length 86;

Matches 17; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Qy 1 AXAAEAAEKA--AKYAAEAAEAKAKAYA 25

Do

47 AKEKKEKAAEAKYKAAKAKAA 74

Do

RESULT 5

US-09-816-989A-6

; Sequence 6, Application US/09816989A

; Patent No. 6800287

; GENERAL INFORMATION:

; APPLICANT: Gad, Alexander

; APPLICANT: Lis, Doris

; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

; TITLE OF INVENTION: AND FOR THERAPEUTIC USE

; FILE REFERENCE: 2609/60807-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/816, 989A

; PRIOR APPLICATION NUMBER: 60/101, 693

; PRIOR FILING DATE: 1998-09-25

; PRIOR APPLICATION NUMBER: PCT/US99/22402

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SEQ ID NO 6

; LENGTH: 86

; PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide

; US-09-816-989A-6

Query Match Best Local Similarity 58.6%; Score 61.5; DB 4; Length 86;

Matches 17; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Qy 1 AXAAEAAEKA--AKYAAEAAEAKAKAYA 25
Db 47 AKEKKEKAAEAKYKAAKAKAA 74

; LENGTH: 86

; PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide

; US-08-03-025-16

Query Match Best Local Similarity 58.6%; Score 61.5; DB 4; Length 86;

Matches 16; Application US/08303025

; Patent No. 5614494

; GENERAL INFORMATION:

; APPLICANT: Wakefield, Thomas W.

; APPLICANT: Andrews, Philip C.

; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND

; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN

; TITLE OF INVENTION: ANTICOAGULATION REVERSAL

; NUMBER OF SEQ ID NOS: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Benita J. Rohm, Esq.

; STREET: 150 West Jefferson, Suite 2500

; CITY: Detroit

; STATE: Michigan

; COUNTRY: United States of America

; ZIP: 48226-4415

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy diskette 3.5" 1.44MB

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: MS-DOS v.6.22

; SOFTWARE: Worrell 6.1; ASCII (DOS) Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/303, 025

; FILING DATE: 09-SEPT-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/06829

; FILING DATE: 14-AUG-1992

; APPLICATION NUMBER: US/08/152, 488

; FILING DATE: 12-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Rohm, Benita J.

REFERENCE/DOCKET NUMBER: 7WH-060548-00231
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-496-7622
 TELEFAX: 313-496-8454
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: N/A
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 DOCUMENT NUMBER: PCT/US92/08059
 FILING DATE: 14-AUG-1993
 US-08-303-025-16

Query Match 58.1%; Score 61; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 0.067;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 BAAEKAAYAEEAEKAAX 24
 Db 1 EAAKKAAGCAKKAAGKA 21

RESULT 7
 US-08-436-703B-4

Sequence 4 Application US/08436703B
 Patent No. 591961
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR
 HEPARIN AND LOW MOLECULAR
 WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 6601 Woodward Avenue
 STREET: Suite 1525
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America
 ZIP: 48225

COMPUTER READABLE FORM:
 COMPUTER TYPE: FLOPPY disk 1.44Mb, 3.5"
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6;
 SOFTWARE: ASCII (DOS) Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436,703B
 FILING DATE: 08-MAY-1995
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: N/A
 FILING DATE: N/A
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REGISTRATION NUMBER: 28,664
 REFERENCE/DOCKET NUMBER: 7WK-060548-00233
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-965-1976
 TELEFAX: 313-965-1951
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids

Query Match 58.1%; Score 61; DB 2; Length 33;
 Best Local Similarity 66.7%; Pred. No. 0.067;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 BAAEKAAYAEEAEKAAX 24
 Db 1 EAAKKAAGCAKKAAGKA 21

RESULT 8
 US-09-489-039A-13565

Sequence 13565, Application US/09489039A
 Patent No. 6610356
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 - PRIORITY APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 13565
 LENGTH: 469
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-13565

Query Match 58.1%; Score 61; DB 4; Length 469;
 Best Local Similarity 62.5%; Pred. No. 1.3;
 Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Qy 2 XAAEKAAYAEEAEKAAXA 25
 Db 301 KAAAEKAAYAEEAEKAADKAATAA 324

RESULT 9
 US-09-340-736E-9

Sequence 9, Application US/09340736E
 Patent No. 6489446
 GENERAL INFORMATION:
 APPLICANT: ROTSTEIN, ASER
 APPLICANT: ROTSTEIN, ASER
 APPLICANT: KEELEY, FRED
 APPLICANT: ROTSTEIN, STEVEN
 TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
 TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
 FILE REFERENCE: 041982/0110
 CURRENT APPLICATION NUMBER: US/09/340,736E
 CURRENT FILING DATE: 1999-06-29
 PRIOR APPLICATION NUMBER: 08/911,364
 PRIOR FILING DATE: 1997-08-07
 PRIOR APPLICATION NUMBER: 60/023,552
 PRIOR FILING DATE: 1996-08-07
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 9
 LENGTH: 117
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:

RESULT 14
US-09-364-662-11
; Sequence 11, Application US/09964662
; Patent No. 6765086
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-662-11

RESULT 15
Query Match 57.6%; Score 60.5; DB 4; Length 199;
Best Local Similarity 58.6%; Pred. No. 0.59;
Matches 17; Conservative 3; Mismatches 4; Indels 5; Gaps 1;
QY 1 AXAAEAKAKY----AXAAEAKAKAX 24
Db 37 AQAAAAKAKYGVGTPAAAKAKAA 65

RESULT 16
US-09-340-736E-2
; Sequence 2, Application US/09340736E
; Patent No. 6489446
; GENERAL INFORMATION:
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: KEELEY, FRED
; APPLICANT: ROTHSTEIN, STEVEN J.
; TITLE OF INVENTION: SELF ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
; TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0110
; CURRENT APPLICATION NUMBER: US/09/340,736E
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 08/911,364
; PRIOR FILING DATE: 1997-08-07
; PRIOR APPLICATION NUMBER: 60/023,552
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Polypeptide
; US-09-964-662-2

RESULT 17
US-08-911-364-2
; Sequence 2, Application US/08911364
; Patent No. 5969106
; GENERAL INFORMATION:
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: KEELEY, Fred W.
; APPLICANT: ROTHSTEIN, Steven J.
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
; TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
; NUMBER OF SEQ ID NOS: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC-compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,552
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,552
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 041082/0104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; RESULT 16
US-09-964-662-2

```

; STRANDEDNESS: linear
; MOLECULE TYPE: Peptide
; US-08-911-364-2

Query Match      57.6%;  Score 60.5;  DB 2;  Length 201;
Best Local Similarity 58.6%;  Pred. No. 0..6;  Mismatches 3;  Indels 4;  Gaps 1;
Matches 17;  Conservative 3;  Mismatches 4;  Indels 5;  Gaps 1;

Qy   1 AXAAEAKAKY----AEEAEKAKX 24
Db   38 AQAAGAAKAKYGVGTPAAAKAAKAA 66

RESULT 18
US-09-961-403-8
; Sequence 8, Application US/09961403
; Patent No. 6780594

GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFFT, BERTHOLD
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789

CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 730
TYPE: PRT
ORGANISM: Homo sapiens

US-09-961-403-8

Query Match      57.6%;  Score 60.5;  DB 4;  Length 730;
Best Local Similarity 58.6%;  Pred. No. 2.5;  Mismatches 3;  Indels 5;  Gaps 1;
Matches 17;  Conservative 3;  Mismatches 4;  Indels 5;  Gaps 1;

Qy   1 AXAAEAKAKY----AEEAEKAKX 24
Db   415 AQAAGAAKAKYGVGTPAAAKAAKAA 469

RESULT 19
US-08-911-364-1
; Sequence 1, Application US/08911364
; Patent No. 5369106
; GENERAL INFORMATION:
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: KEELY, Fred W.
; APPLICANT: ROTHSTEIN, Steven J.
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIORITY NUMBER: 08/911,364
PRIORITY FILING DATE: 1997-08-07
PRIORITY APPLICATION NUMBER: 60/023,552
PRIORITY FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 731
TYPE: PRT
ORGANISM: Homo sapiens

US-09-961-403-8

Query Match      57.6%;  Score 60.5;  DB 4;  Length 731;
Best Local Similarity 58.6%;  Pred. No. 2.5;  Mismatches 3;  Indels 4;  Gaps 1;
Matches 17;  Conservative 3;  Mismatches 4;  Indels 5;  Gaps 1;

Qy   1 AXAAEAKAKY----AEEAEKAKX 24
Db   415 AQAAGAAKAKYGVGTPAAAKAAKAA 443

RESULT 20
US-09-911-364-1
; Sequence 1, Application US/09940736E
; Patent No. 6489446
; GENERAL INFORMATION:
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: KEELY, Fred W.
; APPLICANT: ROTHSTEIN, Steven J.
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIORITY NUMBER: 08/911,364
PRIORITY FILING DATE: 1997-08-07
PRIORITY APPLICATION NUMBER: 60/023,552
PRIORITY FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 731
TYPE: PRT
ORGANISM: Homo sapiens

US-09-961-403-8

Query Match      57.6%;  Score 60.5;  DB 4;  Length 731;
Best Local Similarity 58.6%;  Pred. No. 2.5;  Mismatches 3;  Indels 4;  Gaps 1;
Matches 17;  Conservative 3;  Mismatches 4;  Indels 5;  Gaps 1;

Qy   1 AXAAEAKAKY----AEEAEKAKX 24
Db   415 AQAAGAAKAKYGVGTPAAAKAAKAA 443

RESULT 21
US-09-954-652-1
; Sequence 1, Application US/09964662
; Patent No. 6760586
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
TITLE OF INVENTION: OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0112

APPLICATION NUMBER: US/09/911,364
FILING DATE: 07-AUG-1997

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CURRENT APPLICATION NUMBER: US/09/964,662
 CURRENT FILING DATE: 2003-05-08
 PRIOR APPLICATION NUMBER: 09/340,736
 PRIOR FILING DATE: 1999-06-29
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 731
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-964-662-1

RESULT 22
 US-08-464-700-2
 Matches 17; Conservative 58.6%; Pred. No. 2.5; Mismatches 3; Indels 4; Gaps 5; Gaps 1;
 QY 1 AXAAEAKAAKAY----AAEAEKAAXAX 24
 Db 415 AQAAGAAKAAKAYGVGVGPAAAKAAKAA 443

Query Match 57.6%; Score 60.5; DB 4; Length 731;
 Best Local Similarity 58.6%; Pred. No. 2.5; Mismatches 3; Indels 4; Gaps 5; Gaps 1;
 Matches 17; Conservative 58.6%; Pred. No. 2.5; Mismatches 3; Indels 4; Gaps 5; Gaps 1;

GENERAL INFORMATION:
 APPLICANT: WEISS, ANTHONY S
 APPLICANT: MARTIN, STEPHEN L
 TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Howson and Howson
 STREET: Spring House Corporate Cntr, PO Box. 457
 CITY: Spring House
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19477

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,700
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AJ PL6520
 FILING DATE: 22-DEC-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AJ PL9661
 FILING DATE: 28-JUN-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU93/00655
 FILING DATE: 16-DEC-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: GHG3USA

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9200
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 733 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-464-700-2

Query Match 57.6%; Score 60.5; DB 3; Length 733;
 Best Local Similarity 58.6%; Pred. No. 2.6; Mismatches 3; Indels 4; Gaps 5; Gaps 1;

RESULT 23
 US-09-869-875-7
 Sequence 7, Application US/09869875
 Patent No. 652156
 GENERAL INFORMATION:
 APPLICANT: Siebenkotten, Gregor
 APPLICANT: Christine, Rainer
 TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC AC
 FILE REFERENCE: 30430.1USWO
 CURRENT APPLICATION NUMBER: US/09/869,875
 CURRENT FILING DATE: 2001-07-06
 PRIOR APPLICATION NUMBER: PCT/DE00/00061
 PRIOR FILING DATE: 2000-01-03
 PRIOR APPLICATION NUMBER: DE 199 00 513.3
 PRIOR FILING DATE: 1999-01-08
 PRIOR APPLICATION NUMBER: DE 199 33 939.2
 PRIOR FILING DATE: 1999-07-20
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 7
 LENGTH: 67
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: PNA-NLS

US-09-869-875-7

Query Match 56.7%; Score 59.5; DB 4; Length 67;
 Best Local Similarity 61.5%; Pred. No. 0.24; Mismatches 6; Indels 3; Gaps 1; Gaps 1;
 Matches 16; Conservative 61.5%; Pred. No. 0.24; Mismatches 6; Indels 3; Gaps 1; Gaps 1;

QY 1 AXAAEAKAYA-EAAEKAAXAX 25
 Db 4 AEEBAAEAAEAAEAAEAAEAAEAA 29

RESULT 24
 US-09-405-743A-2
 Sequence 2, Application US/09405743A
 Patent No. 651938
 GENERAL INFORMATION:
 APPLICANT: Yeda Research and Development Co., Ltd.
 TITLE OF INVENTION: GLATTRAMER ACETATE MOLECULAR WEIGHT MARKERS
 FILE REFERENCE: 60807-A
 CURRENT APPLICATION NUMBER: US/09/405,743A
 CURRENT FILING DATE: 1999-09-24
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 45
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 OTHER INFORMATION: Peptide
 US-09-405-743A-2

Query Match 56.2%; Score 59; DB 4; Length 45;
 Best Local Similarity 58.3%; Pred. No. 0.18; Mismatches 7; Indels 0; Gaps 0;
 Matches 14; Conservative 58.3%; Pred. No. 0.18; Mismatches 7; Indels 0; Gaps 0;

QY 2 XAAEAKAYA-EAAEKAAXAX 25
 Db 18 KAAEAKAKAYEKAAEKAKEA 41

RESULT 25
 US-09-816-989A-2
 Sequence 2, Application US/09816989A
 Patent No. 6800287
 GENERAL INFORMATION:
 APPLICANT: Gad, Alexander
 APPLICANT: Lis, Doris
 TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
 FILE REFERENCE: 2609/60807-A-PCT-US
 CURRENT APPLICATION NUMBER: US/09/816, 989A
 CURRENT FILING DATE: 2001-03-23
 CURRENT FILING DATE: 1998-09-25
 PRIORITY NUMBER: US/09/816, 989A
 PRIORITY FILING DATE: 1999-09-24
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 45
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
 US-09-816-989A-2

Query Match 56.2%; Score 59; DB 4; Length 45;
 Best Local Similarity 58.3%; Pred. No. 0.18;
 Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 2 XAEEAAEKAKYAAEAAEKAKAXA 25
 DB 18 KAAEAKKAKAKYEEKAEEKAEEKA 41

RESULT 26
 US-09-405-743A-7
 Sequence 7, Application US/09405743A
 Patent No. 651438
 GENERAL INFORMATION:
 APPLICANT: Yeda Research and Development Co., Ltd
 TITLE OF INVENTION: GLATRIMER ACETATE MOLECULAR WEIGHT MARKERS
 FILE REFERENCE: 60807-A
 CURRENT APPLICATION NUMBER: US/09/405, 743A
 CURRENT FILING DATE: 1999-09-24
 CURRENT FILING DATE: 1999-09-24
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 109
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 OTHER INFORMATION: PEPTIDE
 US-09-405-743A-7

Query Match 56.2%; Score 59; DB 4; Length 109;
 Best Local Similarity 56.0%; Pred. No. 0.47;
 Matches 14; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 AXAEEAAEKAKYAAEAAEKAKAXA 25
 DB 82 AEAKEAKKAKAKYAAEAAEKAKAEA 106

RESULT 27
 US-09-816-989A-7
 Sequence 7, Application US/09816989A
 Patent No. 6800287
 GENERAL INFORMATION:
 APPLICANT: Gad, Alexander
 APPLICANT: Lis, Doris
 TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
 FILE REFERENCE: 2609/60807-A-PCT-US
 CURRENT APPLICATION NUMBER: US/09/816, 989A
 CURRENT FILING DATE: 2001-03-23
 PRIORITY NUMBER: 601101, 693
 PRIORITY FILING DATE: 1998-09-25
 PRIORITY NUMBER: PCT/US99/22402
 PRIORITY FILING DATE: 1999-09-24
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 45
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
 US-09-816-989A-7

Query Match 56.2%; Score 59; DB 4; Length 109;
 Best Local Similarity 56.0%; Pred. No. 0.47;
 Matches 14; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 AXAEEAAEKAKYAAEAAEKAKAXA 25
 DB 82 AEAKEAKKAKAKYAAEAAEKAKAEA 106

RESULT 28
 US-09-405-743A-5
 Sequence 5, Application US/09405743A
 Patent No. 651438
 GENERAL INFORMATION:
 APPLICANT: Yeda Research and Development Co., Ltd.
 TITLE OF INVENTION: GLATRIMER ACETATE MOLECULAR WEIGHT MARKERS
 FILE REFERENCE: 60807-A
 CURRENT APPLICATION NUMBER: US/09/405, 743A
 CURRENT FILING DATE: 1999-09-24
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 5
 LENGTH: 77
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 OTHER INFORMATION: PEPTIDE
 US-09-405-743A-5

Query Match 55.2%; Score 58; DB 4; Length 77;
 Best Local Similarity 51.6%; Pred. No. 0.44;
 Matches 16; Conservative 4; Mismatches 5; Indels 6; Gaps 1;
 QY 1 AXAEEAAEKAK-----YAAEAEKAAGAXA 25
 DB 10 AVAKKEAKKAKAKYAAEAKKAKAEA 40

RESULT 29
 US-09-816-989A-5
 Sequence 5, Application US/09816989A
 Patent No. 6800287
 GENERAL INFORMATION:
 APPLICANT: Gad, Alexander
 APPLICANT: Lis, Doris
 TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
 FILE REFERENCE: 2609/60807-A-PCT-US
 CURRENT APPLICATION NUMBER: US/09/816, 989A
 CURRENT FILING DATE: 2001-03-23
 PRIORITY NUMBER: 601101, 693
 PRIORITY FILING DATE: 1998-09-25
 PRIORITY NUMBER: PCT/US99/22402
 PRIORITY FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Version 3.1
 SEQ ID NO 5
 LENGTH: 77
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
 US-09-816-989A-5

Query Match 55.2%; Score 58; DB 4; Length 77;
 Best Local Similarity 51.6%; Pred. No. 0.44; Mismatches 5; Indels 1; Gaps 1;
 Matches 16; Conservative 4; Mismatches 5; Indels 6; Gaps 1;
 Qy 1 AXAERAEKAAK----YAAEAEKAKLXA 25
 Db 10 AYAKKAEKAAKKAEEAKAYKAEEAKKKAKAEA 40

RESULT 30

US-09-44-529-2
 Sequence 2, Application US/09344529
 PATENT NO. 6429393
 GENERAL INFORMATION:

APPLICANT: Hsu, Choy L.
 APPLICANT: HSC Research and Development Limited Partnership

TITLE OF INVENTION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
 FILE REFERENCE: 016252-002620US
 CURRENT APPLICATION NUMBER: US/09/344,529

CURRENT FILING DATE: 1999-06-24
 EARLIER APPLICATION NUMBER: US 60/090,794
 EARLIER FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 92
 TYPE: PRT
 ORGANISM: Myoxocephalus scorpius

Query Match 55.2%; Score 58; DB 4; Length 92;
 Best Local Similarity 60.0%; Pred. No. 0.53; Mismatches 7; Indels 0; Gaps 0;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AXAERAEKAAKYYAAEAKAKAXA 25
 Db 3 AAKAAEAAKAAAMAAKAAEAKTAA 27

RESULT 31

US-09-902-540-13678
 Sequence 13678, Application US/09902540
 Patent No. 6833447
 GENERAL INFORMATION:

APPLICANT: Goldblatt, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.

APPLICANT: Wiegard, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10 (15849)B
 CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 13678
 LENGTH: 325
 TYPE: PRT
 ORGANISM: Myxococcus xanthus

US-09-902-540-13678

Query Match 54.8%; Score 57.5; DB 4; Length 325;
 Best Local Similarity 61.5%; Pred. No. 2.6; Mismatches 5; Indels 1; Gaps 1;
 Matches 16; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AXAERAEKAKYAE-AEKAAKAYA 25
 Db 20 AAKAAEAAKAKAAEAAKTTAERA 45

RESULT 32

US-08-303-025-12
 Sequence 12, Application US/08303025
 PATENT NO. 5614494
 GENERAL INFORMATION:

APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.

TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 NUMBER OF INVENTION: ANTICOGULATION REVERSAL
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 150 West Jefferson, Suite 2500
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America
 ZIP: 48226-4415

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS v.6.22
 SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/303,025
 FILING DATE: 08-SEPT-1994
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/06829
 FILING DATE: 14-AUG-1992
 APPLICATION NUMBER: US 08/152,488

FILING DATE: 12-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.

REFERENCE/DOCKET NUMBER: 7WH-060548-00231
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-496-7622
 TELEFAX: 313-496-8454

INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A

TOPOLOGY: N/A
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE: N/A
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993

Query Match 54.3%; Score 57; DB 1; Length 28;
 Best Local Similarity 56.5%; Pred. No. 0.19; Mismatches 4; Indels 0; Gaps 0;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 XAEAEKAKYAAEAKAKAX 24

Db 1 PAKKAKKAKKAKKAKKAKKAA 23

US-09-902-540-13678

RESULT 33 US-08-436-703B-1

Sequence 1, Application US/08436703B
 Patent No. 5919761
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR
 TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
 TITLE OF INVENTION: WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J, Rohm, Esq.
 STREET: 6601 Woodward Avenue
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America
 ZIP: 48226
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6,
 SOFTWARE: ASCII (DOS) text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436,703B
 FILING DATE: 08-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: N/A
 FILING DATE: N/A
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REGISTRATION NUMBER: 2B, 664
 REFERENCE/DOCKET NUMBER: 7Wk-060548-00233
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-965-1976
 TELEX/FAX: 313-965-1951
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: N/A
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 MOLECULE TYPE: peptide
 TOPOLOGY: N/A
 ORIGIN SOURCE:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: N/A
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 US-08-436-703B-1

Query Match 54.3%; Score 57; DB 2; Length 28;
 Best Local Similarity 56.5%; Pred. No. 0.19; 4; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 XAEEAKKAKYAAEAEKAKAX 24
 Db 1 :|:|:|||:|:|||:|||:
 1 PAKKAKKAKKAKKAKKAKKA 23

RESULT 34 US-08-152-488-10

Sequence 10, Application US/08152488
 Patent No. 5534619
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J, Rohm, Esq.
 STREET: 512 Springfield Avenue
 CITY: Cranford
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07016-1811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6; ASCII (DOS) text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/152,488
 FILING DATE: 12-NOV-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REGISTRATION NUMBER: 2B, 664
 REFERENCE/DOCKET NUMBER: RM,7WG
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-276-3344
 TELEX/FAX: 908-276-5543
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: N/A
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 US-08-152-488-10

Query Match 54.3%; Score 57; DB 1; Length 29;
 Best Local Similarity 56.5%; Pred. No. 0.2; 4; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 XAEEAKKAKYAAEAEKAKAX 24
 Db 5 AAKKAKKAKKAKKAKKAKKA 27

RESULT 35 US-08-152-488-11

Sequence 11, Application US/08152488
 Patent No. 5534619
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J, Rohm, Esq.
 STREET: 512 Springfield Avenue
 CITY: Cranford
 STATE: New Jersey
 COUNTRY: United States of America

ZIP: 07016-1811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/152,488
 FILING DATE: 12-NOV-1993
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REGISTRATION NUMBER: 28,664
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 MOLECULE TYPE: peptide
 STRANDEDNESS: N/A
 TOPOLOGY: N/A
 ORIGINAL SOURCE:
 ORGANISM: N/A
 AUTHORS: N/A
 TITLE: N/A
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 US-08-152-488-11

RESULT 36
 Query Match 54.3%; Score 57; DB 1; Length 29;
 Best local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 2 XAAEAKKAQYAAEAKAKAX 24
 Db 5 AAKKAKKAQAKKAKKAKKAKKA 27

RESULT 36
 Query Match 54.3%; Score 57; DB 1; Length 29;
 Best local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 2 XAAEAKKAQYAAEAKAKAX 24
 Db 5 AAKKAKKAQAKKAKKAKKAKKAKKA 27

RESULT 36
 Query Match 54.3%; Score 57; DB 1; Length 29;
 Best local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 2 XAAEAKKAQYAAEAKAKAX 24
 Db 5 AAKKAKKAQAKKAKKAKKAKKAKKA 27

RESULT 37
 US-08-030-025-10
 Sequence 10, Application US/080303025
 Patent No. 561494
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 150 West Jefferson, Suite 2500
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America

RESULT 37
 US-08-030-025-10
 Sequence 10, Application US/080303025
 Patent No. 561494
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 150 West Jefferson, Suite 2500
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America

RESULT 37
 US-08-030-025-10
 Sequence 10, Application US/080303025
 Patent No. 561494
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 150 West Jefferson, Suite 2500
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/152,488
 FILING DATE: 12-NOV-1993
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REFERENCE/DOCKET NUMBER: 7WH-060548-00231

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6; ASCII (DOS) Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/152,488
 FILING DATE: 12-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REFERENCE/DOCKET NUMBER: 7WH-060548-00231

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-496-7622
 TELEFAX: 313-496-8454
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 MOLECULE TYPE: peptide
 ORGANISM: N/A
 ORIGINAL SOURCE:
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 US-08-303-025-10

Query Match 54.3%; Score 57; DB 1; Length 29;
 Best Local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 XAEAEKAAYAEEAEKAAX 24
 Db 5 AAKKAKKKAKKKAKKKAA 27

RESULT 38
 US-08-303-025-11
 Sequence 11; Application US/08303025
 Patent No. 5614494
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 150 West Jefferson, Suite 2500
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America
 ZIP: 48226-4115
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
 OPERATING SYSTEM: MS-DOS v.6.22
 SOFTWARE: Wordperfect 6.1; ASCII (DOS)Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/303,025
 FILING DATE: 08-SEPT-1994
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/06829
 FILING DATE: 14-AUG-1992
 APPLICATION NUMBER: US 08/152,488
 FILING DATE: 12-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REFERENCE/DOCKET NUMBER: 7WH-060548-00231
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-496-7622
 TELEFAX: 313-496-8454
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 MOLECULE TYPE: peptide
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 US-08-303-025-13

RESULT 39
 US-08-303-025-13
 Sequence 13; Application US/08303025
 Patent No. 5614494
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 150 West Jefferson, Suite 2500
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America
 ZIP: 48226-4115
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS v.6.22
 SOFTWARE: Wordperfect 6.1; ASCII (DOS)Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/152,488
 FILING DATE: 12-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REFERENCE/DOCKET NUMBER: 7WH-060548-00231
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-496-7622
 TELEFAX: 313-496-8454
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 MOLECULE TYPE: peptide
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 US-08-303-025-13

Query Match 54.3%; Score 57; DB 1; Length 29;
 Best Local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 XAAEAKKAAYAAEAKAKAX 24
 Db 5 AAKKAKKAACKKAKKAKKAA 27

RESULT 40
 Sequence 14, Application US/08303025
 Patent No. 5614494
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 150 West Jefferson, Suite 2500
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America
 ZIP: 48226-4415
 COMPUTER READABLE FORM:
 MEDIUM TYPE: /FLOPPY diskette 3.5" 1.44MB
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS v.6.22
 SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/303,025
 FILING DATE: 08-SEP-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/06829
 FILING DATE: 14-AUG-1992
 APPLICATION NUMBER: US 08/1152,488
 FILING DATE: 12-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REFERENCE/DOCKET NUMBER: TWH-060548-00231
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-496-7622
 TELEFAX: 313-496-8454
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: N/A
 TOPOLOGY: No. 5721212 Relevant
 MOLECULE TYPE: peptide
 MOLECULAR SOURCE:
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 US-08-303-025-14

Query Match 54.3%; Score 57; DB 1; Length 29;
 Best Local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 XAAEAKKAAYAAEAKAKAX 24
 Db 5 AAKKAKKAACKKAKKAKKAA 27

RESULT 41
 Sequence 10, Application US/08677304
 Patent No. 5721212
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 512 Springfield Avenue
 CITY: Crawford
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07016-1811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6; ASCII (DOS)Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/677,304
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/152,488
 FILING DATE: 12-NOV-1993
 APPLICATION NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REGISTRATION NUMBER: 28,664
 REFERENCE/DOCKET NUMBER: RM-7WQ
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-276-3344
 TELEFAX: 908-276-5543
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: No. 5721212 Relevant
 TOPOLOGY: No. 5721212 Relevant
 MOLECULE TYPE: peptide
 MOLECULAR SOURCE:
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 US-08-677-304-10

Query Match 54.3%; Score 57; DB 1; Length 29;
 Best Local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 XAAEAKKAAYAAEAKAKAX 24
 Db 5 AAKKAKKAACKKAKKAKKAA 27

RESULT 42
 Sequence 11, Application US/08677304
 Patent No. 5721212
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.

APPLICANT: Andrews, Philip C.
 ADDRESS: Benita J. Rohm, Esq.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 NUMBER OF SEQUENCES: 13
 COUNTRY: United States of America
 ZIP: 07016-1811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6; ASCII (DOS) Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/677,304
 FILING DATE: 14-AUG-1993
 CLASSIFICATION: 530
 PRIORITY DATA:
 APPLICATION NUMBER: US/08/1152,488
 FILING DATE: 12-NOV-1993
 APPLICATION NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rohm, Benita J.
 REGISTRATION NUMBER: 28,664
 REFERENCE/DOCKET NUMBER: RM-7WG
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-276-3344
 TELEFAX: 908-276-5543
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: No. 5721212 Relevant
 TOPOLOGY: No. 5721212 Relevant
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: N/A
 PUBLICATION INFORMATION:
 AUTHORS: N/A
 TITLE: N/A
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: PCT/US92/08069
 FILING DATE: 14-AUG-1993
 US-08-677-304-11

Query Match 54.3%; Score 57; DB 1; Length 29;
 Best Local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

RESULT 43
 US-08-677-304-12
 Sequence 12, Application US/08677304
 Patent No. 577212
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 APPLICANT: James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
 TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 6601 Woodward Avenue
 STREET: Suite 1525
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America

Query Match 54.3%; Score 57; DB 1; Length 29;
 Best Local Similarity 56.5%; Pred. No. 0.2;
 Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

RESULT 44
 US-08-436-703B-3
 Sequence 3, Application US/08436703B
 Patent No. 591961
 GENERAL INFORMATION:
 APPLICANT: Wakefield, Thomas W.
 APPLICANT: Andrews, Philip C.
 APPLICANT: Stanley, James C.
 APPLICANT: James C.
 TITLE OF INVENTION: NOVEL PEPTIDES FOR
 TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
 TITLE OF INVENTION: WEIGHT HEPARIN
 TITLE OF INVENTION: ANTICOAGULATION REVERSAL
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Benita J. Rohm, Esq.
 STREET: 6601 Woodward Avenue
 STREET: Suite 1525
 CITY: Detroit
 STATE: Michigan
 COUNTRY: United States of America

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Om protein - protein search, using sw model
Run on: July 11, 2005, 09:46:35 : Search time 159 Seconds
(without alignments)
60.744 Million cell updates/sec

Title: SBQ1
perfect score: 105

Sequence: 1 axaaeakakayaaeakakaxa 25

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1726218 seqs, 386331768 residues

Total number of hits satisfying chosen parameters: 1726218

Minimum DB seq length: 0
Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
US-10-177-725-42
; Sequence 42, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMSAMS
; CURRENT APPLICATION NUMBER: US/10/177-725
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 42
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-177-725-42

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Sequence 92, Appl
Sequence 42, Appl
Sequence 92, Appl
Sequence 12005, Appl
Sequence 55748, Appl
Sequence 21, Appl
Sequence 24, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 89, Appl
Sequence 90, Appl
Sequence 41, Appl
Sequence 91, Appl
Sequence 41, Appl
Sequence 55, Appl
Sequence 105, Appl
Sequence 55, Appl
Sequence 53, Appl
Sequence 103, Appl
Sequence 54, Appl
Sequence 104, Appl
Sequence 102, Appl
Sequence 49, Appl
Sequence 52, Appl
Sequence 102, Appl
Sequence 51, Appl
Sequence 101, Appl
Sequence 51, Appl
Sequence 101, Appl
Sequence 47, Appl

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15 64 61.0 104 15 US-10-177-725-90 Sequence 89, Appl
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35 63 60.0 104 15 US-10-177-725-52 Sequence 52, Appl
36 63 60.0 104 15 US-10-177-725-102 Sequence 102, Appl
37 63 60.0 104 14 US-10-177-725-49 Sequence 49, Appl
38 63 60.0 104 14 US-10-177-725-49 Sequence 103, Appl
39 63 60.0 104 15 US-10-177-725-49 Sequence 49, Appl
40 63 60.0 104 15 US-10-177-725-49 Sequence 99, Appl
41 63 60.0 104 14 US-10-177-725-51 Sequence 51, Appl
42 63 60.0 104 15 US-10-177-725-101 Sequence 101, Appl
43 63 60.0 104 15 US-10-177-725-51 Sequence 51, Appl
44 63 60.0 104 15 US-10-177-725-49-101 Sequence 101, Appl
45 63 60.0 104 14 US-10-177-725-47 Sequence 47, Appl

RESULT 2 US-10-177-725-92

; Sequence 92, Application US/10177725

; Publication No. US20030143562A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, David

; APPLICANT: Bogenberger, Jakob M.

; SEQ ID NO: 42

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE: OTHER INFORMATION: synthetic

; NAME/KEY: MISC_FEATURE

; LOCATION: (37).-(68)

; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-60; 63-65, and 67-69 can be any amino acid

US-10-177-725-92

RESULT 3 US-10-333-449-42

; Sequence 42, Application US/10393449

; Publication No. US2003022412A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, David

; APPLICANT: Bogenberger, Jakob M.

; APPLICANT: Peele, Beau R.

; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S

; SEQ ID NO: 92

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE: OTHER INFORMATION: syntetic

; NAME/KEY: MISC_FEATURE

; LOCATION: (37).-(68)

; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-60; 63-65, and 67-69 can be any amino acid

US-10-333-449-42

RESULT 4 US-10-333-449-92

; Sequence 92, Application US/10393449

; Publication No. US2003022412A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, David

; APPLICANT: Bogenberger, Jakob M.

; SEQ ID NO: 92

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE: OTHER INFORMATION: syntetic

; NAME/KEY: MISC_FEATURE

; LOCATION: (37).-(68)

; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-60; 63-65, and 67-69 can be any amino acid

US-10-333-449-92

RESULT 5 US-10-437-963-152005

; Sequence 152005, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(5221)B

US-10-333-449-42

CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 152205
 LENGTH: 827
 TYPE: PRT
 ORGANISM: *oryza sativa*
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4510_52099C.1.pep
 US-10-437-963-152005

Query Match 62.9%; Score 56; DB 16; Length 827;
 Best Local Similarity 54.5%; Pred. No. 4;
 Matches 18; Conservative 4; Mismatches 3; Indels 8; Gaps 1;

RESULT 6
 US-10-202-122A-55748
 ; Sequence 55748, Application US/10282122A
 ; Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haelebeck, Robert
 APPLICANT: Olsen, Kari
 APPLICANT: Zyrkind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trewick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Rosyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELTR0034A
 CURRENT APPLICATION NUMBER: US/10/282,122A.
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-05-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 55748
 LENGTH: 428
 TYPE: PRT
 ORGANISM: *Enterobacter cloacae*
 US-10-282-122A-55748

Query Match 62.4%; Score 65.5; DB 15; Length 428;
 Best Local Similarity 62.1%; Pred. No. 2.2; Matches 18; Conservative 4; Mismatches 2; Indels 5; Gaps 1;

RESULT 7
 US-10-667-004-21
 ; Sequence 21, Application US/10667004
 ; Publication No. US20040126820A1
 GENERAL INFORMATION:
 APPLICANT: INTEL CORPORATION
 APPLICANT: CHAN, Selena
 APPLICANT: SU, Xing
 APPLICANT: YAMAKAWA, Mineo
 TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
 FILE REFERENCE: INTEL1310-1(P14240X)
 CURRENT APPLICATION NUMBER: US/10/667,004
 CURRENT FILING DATE: 2003-03-19
 PRIOR APPLICATION NUMBER: US 10/251,152
 PRIOR FILING DATE: 2002-09-20
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 21
 LENGTH: 28
 TYPE: RT
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 FEATURE:
 OTHER INFORMATION: Synthetic peptide
 US-10-667-004-21

RESULT 8
 US-10-667-004-24
 ; Sequence 24, Application US/10667004
 ; Publication No. US20040126820A1
 GENERAL INFORMATION:
 APPLICANT: INTEL CORPORATION
 APPLICANT: CHAN, Selena
 APPLICANT: SU, Xing
 APPLICANT: YAMAKAWA, Mineo
 TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION
 FILE REFERENCE: INTEL1310-1(P14240X)
 CURRENT APPLICATION NUMBER: US/10/667,004
 CURRENT FILING DATE: 2003-03-19
 PRIOR APPLICATION NUMBER: US 10/251,152
 PRIOR FILING DATE: 2002-09-20
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 24
 LENGTH: 28
 TYPE: RT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide
 US-10-667-004-24

Query Match 61.0%; Score 64; DB 16; Length 28;
 Best Local Similarity 65.2%; Pred. No. 0.17; Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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 DB 210 AAEAAKQAAQEAEKAKAAE 238

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Db      1 AAEAAAEAAAEAAEAA 23
RESULT 9
US-10-177-725-39
; Sequence 39, Application US/10177-725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
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; TYPE: PRT
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; OTHER INFORMATION: synthetic
; US-10-177-725-39

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Db 9 AAEAAAKAA-AAAEEAKAAA 31

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US-10-177-725-40
; Sequence 40, Application US/10177-725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
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; LENGTH: 104
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; FEATURE: 
; OTHER INFORMATION: synthetic
; US-10-177-725-40

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Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
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Db 9 AAEAAAKAA-AAAEEAKAAA 31

RESULT 11
US-10-177-725-89
; Sequence 89, Application US/10177-725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 104
; TYPE: PRT
; FEATURE: 
; OTHER INFORMATION: synthetic
; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
; US-10-177-725-89

Query Match
; Best local Similarity 72.0%; Score 64; DB 14; Length 104;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
Qy 1 AXAERAEEAKKAYAAEAKKAKA 25
Db 9 AAEAAAKAA-AAAEEAKAAA 31

RESULT 12
US-10-177-725-90
; Sequence 90, Application US/10177-725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 104
; TYPE: PRT
; FEATURE: 
; OTHER INFORMATION: synthetic
; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-6
; OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
; US-10-177-725-90

Query Match
; Best local Similarity 72.0%; Score 64; DB 14; Length 104;

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Matches	18;	Conservative	2;	Mismatches	3;	Indels	2;	Gaps	1;	Best Local Similarity	72.0%;	Pred. No.	0.73;	Matches	18;	Conservative	2;	Mismatches	3;	Indels	2;	Gaps	1;						
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RESULT 13														RESULT 15															
US-10-393-449-39														US-10-393-449-89															
; Sequence 39, Application US/10393449														; Sequence 89, Application US/10393449															
; Publication No. US20030224412A1														; Publication No. US20030224412A1															
; GENERAL INFORMATION:														; GENERAL INFORMATION:															
; APPLICANT: Anderson, David														; APPLICANT: Anderson, David															
; APPLICANT: Bogenberger, Jakob M.														; APPLICANT: Bogenberger, Jakob M.															
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S														; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S															
; CURRENT FILING DATE: 2003-03-18														; CURRENT FILING DATE: 2003-03-18															
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; PRIOR FILING DATE: 1999-10-08														; PRIOR FILING DATE: 1999-10-08															
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; PRIOR FILING DATE: 1998-10-08														; PRIOR FILING DATE: 1998-10-08															
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; ORGANISM: Artificial sequence														; ORGANISM: Artificial sequence															
; FEATURE:														; FEATURE:															
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; Sequence 40, Application US/10393449														; Sequence 90, Application US/10393449															
; Publication No. US20030224412A1														; Publication No. US20030224412A1															
; GENERAL INFORMATION:														; GENERAL INFORMATION:															
; APPLICANT: Anderson, David														; APPLICANT: Anderson, David															
; APPLICANT: Bogenberger, Jakob M.														; APPLICANT: Bogenberger, Jakob M.															
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S														; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S															
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; ORGANISM: Artificial sequence														; ORGANISM: Artificial sequence															
; FEATURE:														; FEATURE:															
; OTHER INFORMATION: synthetic														; OTHER INFORMATION: synthetic															
US-10-393-449-40														US-10-393-449-90															
Query Match 61.0%; Score 64; DB 15; Length 104;														Query Match 61.0%; Score 64; DB 15; Length 104;															
Best Local Similarity 72.0%; Pred. No. 0.73; Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;														Best Local Similarity 72.0%; Pred. No. 0.73; Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;															
; Sequence 39, Application US/10393449														; Sequence 89, Application US/10393449															
; Publication No. US20030224412A1														; Publication No. US20030224412A1															
; GENERAL INFORMATION:														; GENERAL INFORMATION:															
; APPLICANT: Anderson, David														; APPLICANT: Anderson, David															
; APPLICANT: Bogenberger, Jakob M.														; APPLICANT: Bogenberger, Jakob M.															
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S														; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S															
; CURRENT FILING DATE: 2003-03-18														; CURRENT FILING DATE: 2003-03-18															
; PRIOR APPLICATION NUMBER: US 10/177,725														; PRIOR APPLICATION NUMBER: US 10/177,725															
; PRIOR FILING DATE: 2002-06-20														; PRIOR FILING DATE: 2002-06-20															
; PRIOR APPLICATION NUMBER: US 09/415,765														; PRIOR APPLICATION NUMBER: US 09/415,765															
; PRIOR FILING DATE: 1999-10-08														; PRIOR FILING DATE: 1999-10-08															
; PRIOR APPLICATION NUMBER: US 09/169,015														; PRIOR APPLICATION NUMBER: US 09/169,015															
; PRIOR FILING DATE: 1998-10-08														; PRIOR FILING DATE: 1998-10-08															
; NUMBER OF SEQ ID NOS: 173														; NUMBER OF SEQ ID NOS: 173															
; SOFTWARE: Patentin version 3.1														; SOFTWARE: Patentin version 3.1															
; SEQ ID NO 40														; SEQ ID NO 90															
; LENGTH: 104														; LENGTH: 104															
; TYPE: PRT														; TYPE: PRT															
; ORGANISM: Artificial sequence														; ORGANISM: Artificial sequence															
; FEATURE:														; FEATURE:															
; OTHER INFORMATION: synthetic														; OTHER INFORMATION: synthetic															
US-10-393-449-40														US-10-393-449-90															
Query Match 61.0%; Score 64; DB 15; Length 104;														Query Match 61.0%; Score 64; DB 15; Length 104;															

FEATURE: OTHER INFORMATION: synthetic

FEATURE: NAME/KEY: MISC_FEATURE

LOCATION: (37)-(68)

OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-61

OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid

US-10-393-449-90

Query Match 61.0%; Score 64; DB 15; Length 104; Best Local Similarity 72.0%; Pred. No. 0.73; Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1; Oy 1 AXAAEAEKAKYAAEAEKAKAXA 25 Db 9 AAAAEAAKAA-AAAEEAAKAA 31

RESULT 17

US-10-177-725-41

; Sequence 41, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SCS
; FILE REFERENCE: A-65900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 41
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic

US-10-177-725-41

Query Match 60.5%; Score 63.5; DB 14; Length 104; Best Local Similarity 72.0%; Pred. No. 0.85; Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1; Oy 1 AXAAEAEKAKYAAEAEKAKAXA 25 Db 6 AAAAAEAAK-AAAEEAAKAA 29

RESULT 18

US-10-177-725-91

; Sequence 91, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SCS
; FILE REFERENCE: A-65900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 41
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic

US-10-393-449-41

Query Match 60.5%; Score 63.5; DB 15; Length 104; Best Local Similarity 72.0%; Pred. No. 0.85; Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1; Oy 1 AXAAEAEKAKYAAEAEKAKAXA 25 Db 6 AAAAAEAAK-AAAEEAAKAA 29

RESULT 19

US-10-393-449-41

; Sequence 41, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SCS
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 41
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic

US-10-393-449-41

Query Match 60.5%; Score 63.5; DB 15; Length 104; Best Local Similarity 72.0%; Pred. No. 0.85; Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1; Oy 1 AXAAEAEKAKYAAEAEKAKAXA 25 Db 6 AAAAAEAAK-AAAEEAAKAA 29

RESULT 20

US-10-393-449-91

; Sequence 91, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SCS
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765

```

; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 91
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: 
; OTHER INFORMATION: synthetic
; FEATURE: 
; NAME/KEY: MISC_FEATURE
; LOCATION: (37).-(68)
; OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59-60
; OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
US-10-393-449-91

Query Match 60.5%; Score 63.5; DB 15; Length 104;
Best Local Similarity 72.0%; Pred. No. 0.85; Matches 18; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
QY 1 AXAAEAEKAAYAABAEKAKAXA 25
Db 6 AAAAAREAAK-AAAAREAAKAAA 29

RESULT 21
US-10-177-725-55
; Sequence 55, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66300-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 55
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: 
; OTHER INFORMATION: synthetic
US-10-177-725-55

Query Match 60.0%; Score 63; DB 14; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.53; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 2 XAAEAEKAAYAABAEKAKAXA 25
Db 4 DAAAREAAK-AAAAREAAKAAA 27

RESULT 22
US-10-177-725-105
; Sequence 105, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-66300-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725

Query Match 60.0%; Score 63; DB 15; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.53; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 2 XAAEAEKAAYAABAEKAKAXA 25
Db 4 DAAAREAAK-AAAAREAAKAAA 27

RESULT 23
US-10-393-449-55
; Sequence 55, Application US/101393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGI-007/CTP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 55
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: 
; OTHER INFORMATION: synthetic
US-10-393-449-55

Query Match 60.0%; Score 63; DB 15; Length 59;
Best Local Similarity 66.7%; Pred. No. 0.53; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 2 XAAEAEKAAYAABAEKAKAXA 25
Db 4 DAAAREAAK-AAAAREAAKAAA 27

RESULT 24
US-10-393-449-105
; Sequence 105, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.

```

APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: RIGL-007CIP3
 CURRENT APPLICATION NUMBER: US/10/393,449
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/177,725
 PRIOR FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: US 09/415,765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169,015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 105
 LENGTH: 59
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (30)..(46)
 OTHER INFORMATION: "Xaa" at positions 30-32, 34-36, 38-39, 41-43, and 45-46 can be a
 OTHER INFORMATION: ny amino acid
 US-10-393-449-105
 Query Match 60.0%; Score 63; DB 15; Length 59;
 Best Local Similarity 66.7%; Pred. No. 0.53; Mismatches 2; Indels 0; Gaps 0;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Qy 2 XAEAAEKAAYAEEAEKAAXA 25
 Db 4 DAAAEAAAKAAEAAKAAEAA 27
 RESULT 25
 US-10-177-725-54
 Sequence 54, Application US/10177725
 Publication No. US20030143562A1
 GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: A-66000-4/RMS/AMS
 CURRENT APPLICATION NUMBER: US/10/177,725
 CURRENT FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: US 09/415,765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169,015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 54
 LENGTH: 67
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 US-10-177-725-54
 Query Match 60.0%; Score 63; DB 14; Length 67;
 Best Local Similarity 66.7%; Pred. No. 0.61; Mismatches 2; Indels 0; Gaps 0;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Qy 2 XAEAAEKAAYAEEAEKAAXA 25
 Db 4 DAAAEAAAKAAEAAKAAEAA 27
 RESULT 27
 US-10-393-449-54
 Sequence 54, Application US/10393449
 Publication No. US20030224412A1
 GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: RIGL-007CIP3
 CURRENT APPLICATION NUMBER: US/10/393,449
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/177,725
 PRIOR FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: US 09/415,765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169,015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 54
 LENGTH: 67
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 US-10-393-449-54
 Query Match 60.0%; Score 63; DB 15; Length 67;
 Best Local Similarity 66.7%; Pred. No. 0.61; Mismatches 2; Indels 6; Indels 0; Gaps 0;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Qy 2 XAEAAEKAAYAEEAEKAAXA 25
 Db 4 DAAAEAAAKAAEAAKAAEAA 27
 RESULT 26
 US-10-177-725-104
 Sequence 54, Application US/10177725
 Publication No. US20030143562A1
 GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: A-66000-4/RMS/AMS
 CURRENT APPLICATION NUMBER: US/10/177,725
 CURRENT FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: US 09/415,765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169,015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 54
 LENGTH: 67
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 US-10-177-725-104
 Query Match 60.0%; Score 63; DB 14; Length 67;
 Best Local Similarity 66.7%; Pred. No. 0.61; Mismatches 2; Indels 6; Indels 0; Gaps 0;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Query Match 60.0%; Score 63; DB 15; Length 75;
 Best Local Similarity 66.7%; Pred. No. 0.69; 2;
 Mismatches 6; Indels 0; Gaps 0;

Qy 2 XAAEAEKAQKAYAAEAEKAAXA 25
 Db 4 DAAAEAAKAQAAKAAXA 27

RESULT 32
 US-10-393-449-103
 Sequence 103, Application US/10393449
 Publication No. US20030224412A1

GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: RIGL-007CIP3
 CURRENT APPLICATION NUMBER: US/10/393, 449
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/177, 725
 PRIOR FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: US 09/415, 765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169, 015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 103
 LENGTH: 75
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (38).(54)
 OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
 US-10-393-449-103

Query Match 60.0%; Score 63; DB 15; Length 75;
 Best Local Similarity 66.7%; Pred. No. 0.69; 2;
 Mismatches 6; Indels 0; Gaps 0;

Qy 2 XAAEAEKAQKAYAAEAEKAAXA 25
 Db 4 DAAAEAAKAQAAKAAXA 27

RESULT 33
 US-10-177-725-52
 Sequence 52, Application US/10177725
 Publication No. US20030143562A1

GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: A-6590-4-RMS/AMS
 CURRENT APPLICATION NUMBER: US/10/177, 725
 CURRENT FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: US 09/415, 765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169, 015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 LENGTH: 83
 TYPE: PRT
 ORGANISM: Artificial sequence

RESULT 34
 US-10-177-725-102
 Sequence 102, Application US/10177725
 Publication No. US20030143562A1

GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: A-6590-4-RMS/AMS
 CURRENT APPLICATION NUMBER: US/10/177, 725
 CURRENT FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: US 09/415, 765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169, 015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 102
 LENGTH: 83
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 NAME/KEY: MISC_FEATURE
 LOCATION: (38).(54)
 OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
 US-10-177-725-102

Query Match 60.0%; Score 63; DB 14; Length 83;
 Best Local Similarity 66.7%; Pred. No. 0.77; 2;
 Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAAEAEKAQKAYAAEAEKAAX 24
 Db 57 AAKAAEAAKAQAAKAAX 80

RESULT 35
 US-10-393-449-52
 Sequence 52, Application US/10393449
 Publication No. US20030224412A1

GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: RIGL-007CIP3
 CURRENT APPLICATION NUMBER: US/10/393, 449
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/177, 725
 PRIOR FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: US 09/415, 765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169, 015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 LENGTH: 83
 TYPE: PRT
 ORGANISM: Artificial sequence

```

; SEQ ID NO: 52
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-393-449-52

; Query Match 60.0%; Score 63; DB 15; Length 83;
; Best Local Similarity 66.7%; Pred. No. 0.77; No. of Mismatches 6; Indels 0; Gaps 0;
; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
; QY 1 AXAEAEKAQKAYAEEAEKAKAX 24
; Db 57 AAKAAAEAAKAAEAAKAAK 80

RESULT 36
US-10-393-449-102
; Sequence 102, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-07CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 102
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (38)..(54)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
; OTHER INFORMATION: ny amino acid
; US-10-393-449-102

Query Match 60.0%; Score 63; DB 15; Length 83;
; Best Local Similarity 66.7%; Pred. No. 0.77; No. of Mismatches 6; Indels 0; Gaps 0;
; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
; QY 1 AXAEAEKAQKAYAEEAEKAKAX 24
; Db 57 AAKAAAEAAKAAEAAKAAK 80

RESULT 37
US-10-177-725-49
; Sequence 49, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-6590-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 102
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (29)..(60)
; OTHER INFORMATION: "Xaa" at positions 29-31, 33-35, 37-38, 40-42, 44-45, 47-49, 51-5
; OTHER INFORMATION: 3, 55-56, and 58-60 can be any amino acid
; US-10-177-725-49

Query Match 60.0%; Score 63; DB 14; Length 88;
; Best Local Similarity 66.7%; Pred. No. 0.82; No. of Mismatches 6; Indels 0; Gaps 0;
; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
; QY 1 AXAEAEKAQKAYAEEAEKAKAX 24
; Db 63 AAKAAAEAAKAAEAAKAAK 86

RESULT 38
US-10-177-725-99
; Sequence 99, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: A-65900-4/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 99
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (29)..(60)
; OTHER INFORMATION: "Xaa" at positions 29-31, 33-35, 37-38, 40-42, 44-45, 47-49, 51-5
; OTHER INFORMATION: 3, 55-56, and 58-60 can be any amino acid
; US-10-177-725-99

Query Match 60.0%; Score 63; DB 14; Length 88;
; Best Local Similarity 66.7%; Pred. No. 0.82; No. of Mismatches 6; Indels 0; Gaps 0;
; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
; QY 1 AXAEAEKAQKAYAEEAEKAKAX 24
; Db 63 AAKAAAEAAKAAEAAKAAK 86

RESULT 39
US-10-393-449-49
; Sequence 49, Application US/10393449
; Publication No. US20030224412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; FILE REFERENCE: RIGL-007CIP3
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 49
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; US-10-177-725-49

Query Match 60.0%; Score 63; DB 14; Length 88;
; Best Local Similarity 66.7%; Pred. No. 0.82; No. of Mismatches 6; Indels 0; Gaps 0;
; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
; QY 1 AXAEAEKAQKAYAEEAEKAKAX 24
; Db 63 AAKAAAEAAKAAEAAKAAK 86

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; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 49
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; US-10-393-449-49

Query Match 60.0%; Score 63; DB 15; Length 88;
Best Local Similarity 66.7%; Pred. No. 0.82; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AXAAEAEKAKYAAEAEKAKAX 24
Db 63 AAKAAAEAAKAAAEAAKAAAK 86

RESULT 40
US-10-393-449-99
; Sequence 99, Application US/10393449
; Publication No. US2003022412A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; CURRENT APPLICATION NUMBER: US/10/393,449
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/177,725
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; PEAK: 100.0% at position 49
; LOCATION: (29)-(60)
; OTHER INFORMATION: "Xaa" at positions 29-31, 33-35, 37-38, 40-42, 44-45, 47-49, 51-5
; OTHER INFORMATION: 3, 55-56, and 58-60 can be any amino acid
; US-10-393-449-99

Query Match 60.0%; Score 63; DB 15; Length 88;
Best Local Similarity 66.7%; Pred. No. 0.82; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AXAAEAEKAKYAAEAEKAKAX 24
Db 63 AAKAAAEAAKAAAEAAKAAAK 86

RESULT 41
US-10-177-725-51
; Sequence 51, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
; CURRENT APPLICATION NUMBER: US/10/177,725
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; PEAK: 100.0% at position 49
; LOCATION: (38)-(54)
; OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be a
; OTHER INFORMATION: ny amino acid
; US-10-177-725-51

Query Match 60.0%; Score 63; DB 14; Length 91;
Best Local Similarity 66.7%; Pred. No. 0.85; Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AXAAEAEKAKYAAEAEKAKAX 24
Db 65 AAKAAAEAAKAAAEAAKAAAK 88

RESULT 43
US-10-393-449-51
; Sequence 51, Application US/10393449
; Publication No. US2003022412A1

```

GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: RIGL-007CIP3
 CURRENT APPLICATION NUMBER: US/10/393,449
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/177,725
 PRIOR FILING DATE: 2002-05-20
 PRIOR APPLICATION NUMBER: US 09/415,765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169,015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 51
 LENGTH: 91
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic

US-10-393-449-51

Query Match 60.0%; Score 63; DB 15; Length 91;
 Best Local Similarity 66.7%; Pred. No. 0.85;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAAEAKAKYAAEAKAKAX 24
 Db 65 AAKAAEAKAAKAAEAKAAK 88

RESULT 44

US-10-393-449-101

Sequence 101, Application US/10393449
 Publication No. US20030224412A1

GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: RIGL-007CIP3
 CURRENT APPLICATION NUMBER: US/10/393,449
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/177,725
 PRIOR FILING DATE: 2002-05-20
 PRIOR APPLICATION NUMBER: US 09/415,765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169,015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 101
 LENGTH: 91
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic

US-10-393-449-101

Query Match 60.0%; Score 63; DB 15; Length 91;
 Best Local Similarity 66.7%; Pred. No. 0.85;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAAEAKAKYAAEAKAKAX 24
 Db 65 AAKAAEAKAAKAAEAKAAK 88

RESULT 45

US-10-177-725-47

Sequence 47, Application US/10177725
 Publication No. US20030143562A1

GENERAL INFORMATION:
 APPLICANT: Anderson, David
 APPLICANT: Bogenberger, Jakob M.
 APPLICANT: Peele, Beau R.
 TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
 FILE REFERENCE: A-66900-4/RMSIAMS
 CURRENT APPLICATION NUMBER: US/10/177,725
 CURRENT FILING DATE: 2002-05-20
 PRIOR APPLICATION NUMBER: US 09/415,765
 PRIOR FILING DATE: 1999-10-08
 PRIOR APPLICATION NUMBER: US 09/169,015
 PRIOR FILING DATE: 1998-10-08
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 47
 LENGTH: 104

TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic

US-10-177-725-47

Query Match 60.0%; Score 63; DB 14; Length 104;
 Best Local Similarity 66.7%; Pred. No. 0.98;
 Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AXAAEAKAKYAAEAKAKAX 24
 Db 79 AAKAAEAKAAKAAEAKAAK 102

Search completed: July 11, 2005, 10:00:02
 Job time : 160 secs

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